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Please find below and/or attached an Office communication concerning this application or proceeding.

	Application No.	Applicant(s)		
Office Anti-us Comment	10/521,721	FREBOURG ET	FREBOURG ET AL.	
Office Action Summary	Examiner	Art Unit		
	Angela Bertagna	1637		
The MAILING DATE of this communication a Period for Reply	ppears on the cover sheet w	ith the correspondence a	ddress	
A SHORTENED STATUTORY PERIOD FOR REF WHICHEVER IS LONGER, FROM THE MAILING - Extensions of time may be available under the provisions of 37 CFR after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory perion. - Failure to reply within the set or extended period for reply will, by stat Any reply received by the Office later than three months after the mail earned patent term adjustment. See 37 CFR 1.704(b).	DATE OF THIS COMMUNI 1.136(a). In no event, however, may a rd will apply and will expire SIX (6) MOI ute, cause the application to become A	CATION. reply be timely filed NTHS from the mailing date of this BANDONED (35 U.S.C. § 133).	•	
Status				
1) Responsive to communication(s) filed on 23	August 2006			
<u> </u>	nis action is non-final.			
3) Since this application is in condition for allow	•	ters, prosecution as to th	ne merits is	
closed in accordance with the practice under	·	*		
Disposition of Claims	,	·		
4)⊠ Claim(s) <u>1-40</u> is/are pending in the application	nn			
4a) Of the above claim(s) <u>1-25 and 40</u> is/are		on		
5) Claim(s) is/are allowed.		•		
6)⊠ Claim(s) <u>26-39</u> is/are rejected.				
7)⊠ Claim(s) <u>26-39</u> is/are objected to.				
8) Claim(s) are subject to restriction and	or election requirement.			
Application Papers				
9)⊠ The specification is objected to by the Examin	ner			
10) ☐ The drawing(s) filed on 18 April 2005 is/are:		cted to by the Examiner		
Applicant may not request that any objection to the	, , , , , , , , , , , , , , , , , , , ,	· ·		
Replacement drawing sheet(s) including the corre	• • • • • • • • • • • • • • • • • • • •		CFR 1.121(d).	
11) The oath or declaration is objected to by the	·	•		
Priority under 35 U.S.C. § 119				
12) Acknowledgment is made of a claim for foreign	gn priority under 35 U.S.C.	§ 119(a)-(d) or (f).	,	
a)⊠ All b)□ Some * c)□ None of: 1.⊠ Certified copies of the priority docume	nts have been received			
2. ☐ Certified copies of the priority docume		Application No		
3. Copies of the certified copies of the pr			l Stage	
application from the International Bure			Glage	
* See the attached detailed Office action for a li	, , , , , , , , , , , , , , , , , , , ,	received.		
	·			
Attachment(s)			•	
1) Notice of References Cited (PTO-892)		Summary (PTO-413)		
2) Notice of Draftsperson's Patent Drawing Review (PTO-948) 3) Information Disclosure Statement(s) (PTO/SB/08)		s)/Mail Date nformal Patent Application		
Paper No(s)/Mail Date <u>1/19/05; 2/22/05</u> .		hibit A, Exhibit B	5	

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DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group III, claims 26-39 and SEQ ID Nos: 3 and 4, in 1. the reply filed on August 23, 2006 is acknowledged. Applicant has traversed the finding of lack of unity between Groups I-III and also the requirement to select a specific primer pair for examination. Regarding the lack of unity between Groups I-III, Applicant argues that, contrary to the Restriction Requirement mailed May 23, 2006, the prior art of Wang et al. (WO 99/58721) does not teach all of the limitations of the instant claim 9, and therefore, the claims possess a special technical feature linking them over the prior art. This argument was not found persuasive, because although Applicant is correct that Wang does not teach all of the elements of claim 9, the prior art of Duponchel et al. (Human Mutation (2001) 17: 61-70) teaches all of the elements of claims 9 and 26. Therefore, since the prior art of Duponchel anticipates the instant claims 9 and 26, the claims lack a special technical feature linking them over the prior art, and a lack of unity requirement is proper. Applicant also traversed the requirement to select a specific primer pair for examination on the grounds that the Office Action did not demonstrate that the claimed sequences are independent inventions. Applicant cites the fact that the sequences have a common function as evidence that they do not constitute separate inventions. This argument was also not found persuasive, because each different primer pair consists of two different nucleic acid sequences that do not share a common structural core (i.e. they are not homologous variants or degenerates). Also, since each primer pair is designed to amplify a different target sequence, the primers do not share a common function. Therefore, as discussed previously, each primer pair constitutes an independent invention, subject to a lack of unity requirement.

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The requirement is still deemed proper and is therefore made FINAL.

Claims 1-25 and 40 and also the non-elected sequences are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on August 23, 2006.

Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

Priority

2. Receipt is acknowledged of papers submitted under 35 U.S.C. 119(a)-(d), which papers have been placed of record in the file.

Information Disclosure Statement

3. It is noted that the IDS filed February 22, 2005 lists several references that are also cited on the IDS filed January 9, 2005. The duplicate citations have been lined through on the IDS filed February 22, 2005 and considered on the IDS filed January 9, 2005.

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Specification

- 4. The disclosure is objected to because of the following informalities:
- (1) The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. The embedded hyperlinks appear on pages 20 and 25.
 - (2) The "Brief Description of the Drawings" heading is missing
- (3) Tables 1 and 3 list nucleic acid sequences greater than 10 nucleotides in length that are not identified by the appropriate SEQ ID NO.

Appropriate correction is required.

Claim Objections

5. Claims 26-39 are objected to because of the following informalities: These claims depend from non-elected claim (claim 9). Incorporation of the limitations of claim 9 into elected claim 26 would correct this problem. Appropriate correction is required.

Claim Rejections - 35 USC § 112 - 1st paragraph (Scope of Enablement)

6. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claim 39 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the

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specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 8 USPQ2d 1400 (CA FC 1988). *Wands* states at page 1404,

"Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in Ex parte Forman. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims."

Enablement issues

The fundamental enablement problem with the instant claim 39 is that the claim is directed to a method of diagnosing any genetic disease or predicting an individual's propensity to develop any genetic disease based solely on a determination of the presence or absence of an unspecified genomic rearrangement, whereas the disclosure does not demonstrate a single example of a positive diagnosis of any disease based solely on the genetic rearrangement screening results.

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The nature of the invention

Claim 39 is drawn to a method of diagnosing a genetic disease or predicting an individual's propensity to develop a genetic disease based solely on a determination of the presence or absence of a genomic rearrangement. The invention is in a class of invention that the CAFC has characterized as "the unpredictable arts such as chemistry and biology." Mycogen Plant Sci., Inc. v. Monsanto Co., 243 F.3d 1316, 1330 (Fed. Cir. 2001).

The breadth of the claims

Claim 39 is broadly drawn to a method of diagnosing *any* genetic disease or predicting an individual's propensity to developing *any* genetic disease based solely on a determination of the presence or absence of an unspecified genomic rearrangement. The specification asserts that the method may be applied to a number of different diseases including: breast cancer, hereditary non-polyposis colorectal cancer (HNPCC), infantile spinal muscular atrophy, schizophrenia, mental retardation, Von Hippel Lindau cancer syndrome, multiple endocrine neoplasia, neurofibromatosis, retinoblastoma, Peutz-Jeghers syndrome, Sotos syndrome, Smith Magenis syndrome, and beta thalassemias (page 50). The range of diseases and conditions encompassed by claim 39 inherently possess radically different etiologies and symptoms and in many cases have no relationship to each other whatsoever. In short, the claims are extremely broad in scope, covering diagnosis of an immense number of diseases based solely on detection of an unspecified genomic rearrangement, whereas the specification fails to positively diagnose even a single disease or condition based solely on the presence or absence of a genomic rearrangement determined using the method of the invention.

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Quantity of Experimentation

The quantity of experimentation in this area is immense, since there is complete variability as to whether or not the observation of a particular genomic rearrangement is sufficient to positively diagnose the individual in the absence of other diagnostic criteria. It would require significant study and experimentation including trials with hundreds of patients to determine that the presence or absence of even a single genomic rearrangement is capable of reliably functioning alone as the diagnostic indicator for a particular disease. This would be an inventive, unpredictable and difficult undertaking in itself, and the efficacy of any of the observed rearrangements as a diagnostic marker for any particular disease would need to be demonstrated in a variety of patients with a statistically significant result. This would require years of inventive effort, with each of the many intervening steps, upon effective reduction to practice, not providing any guarantee of success in the succeeding steps.

Wacholder et al. (J. Natl. Cancer Institute (2004) 96(6): 434-442) notes that in studies of the association of mutations with specific diseases larger studies with 1500 participants have significantly more statistical power than smaller studies (see page 435). So, the quantity of experimentation factor supports the conclusion that a large quantity of experimentation, with the use of many hundreds, perhaps even thousands, of patient samples would be necessary to demonstrate an association between even one of genomic rearrangements and a specific disease disclosed by Applicant. To cover all possible disclosed genomic rearrangements tens of thousands of patient samples would be necessary, and to cover any fraction of the range of the disclosed diseases and conditions, hundreds of thousands of separate patients and the associated analyses would be required. This is a very large amount of experimentation.

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State of the Prior Art

The art teaches that it is entirely unpredictable whether or not genomic rearrangements are associated with a given disease. For example, Charbonnier et al. (Cancer Research (2001) 62: 848-853) analyzed 92 families fulfilling (at least partially) the Amsterdam criteria for hereditary nonpolyposis colorectal cancer (HNPCC) for genomic rearrangements in the MSH2, MLH1, and MSH6 genes (see abstract and Materials & Methods). Although thirteen rearrangements were identified in the MSH2 gene, no genomic rearrangements were found in the MLH1 and MSH6 genes (see abstract). Similarly, Saugier-Veber analyzed twelve genes involved in mental retardation for genomic rearrangements, but only identified three rearrangements (see abstract). These studies highlight the fact that it is highly unpredictable whether or not genomic rearrangements are found in genes suspected to be associated with specific diseases.

Furthermore, the art is replete with evidence that gene association studies are typically wrong. In fact, Lucentini et al (The Scientist (2004) Vol 18) titled his article "Gene Association Studies Typically Wrong" and states "Two recent studies found that typically, when a finding is first published linking a given gene with a complex disease, there is only roughly a one-third chance that studies will reliably confirm the finding (see page 2 of printout)." This is consistent with the teaching of Wacholder et al (J. Natl. Cancer Institute (2004) 96(6): 434-442) who notes, "Too many reports of associations between genetic variants and common cancer sites and other complex diseases are false positives" (see abstract). Ioannidis (Nature genetics (2001) 29:306-309) further supports this conclusion in pointing out the heterogeneity of results among different studies of genetic polymorphisms (see abstract, for example).

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Therefore, the art suggests that the detection of genomic rearrangements is not always correlated with positive disease diagnosis, but rather must be combined with additional test results. The art also suggests that many reported associations between variant polynucleotides may be incorrect, thereby providing support for the conclusion that it is entirely unpredictable whether a given variant gene will function in a diagnostic capacity for a given disease.

Working Examples

The specification contains several working examples were the claimed method is applied to detection of genomic rearrangements (see pages 59-76). However, the nucleic acid samples used in these examples were isolated from patients already diagnosed with a specific disease (colorectal cancer, schizophrenia, etc) rather than an undiagnosed sample, and no indication is given, either in the examples, or elsewhere in the specification that the method outlined in the working examples could be used to positively diagnose even one disease in the absence of additional tests.

Guidance in the Specification

The specification teaches generally that genomic rearrangements may be used to diagnose a number of diseases (page 50). In some instances, specific regions where rearrangements may occur are taught (see page 51 and the working examples, which targeted specific regions as potentially containing genomic rearrangements). However, the specification fails to teach that a positive diagnosis of even one of the disclosed diseases is possible based solely on the presence of a genomic rearrangement. As noted above, the working examples were

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conducted using samples from patients already diagnosed with the particular disesase, and therefore, function as a means of assay validation rather than a means of diagnosing subjects with unknown disease status. Finally, the specification provides no guidance on methods or techniques to demonstrate an association between any specific disease and any specific genomic rearrangement. The specification even fails to provide any discussion or description of the scientific steps necessary to provide evidence that would associate a particular gene or variant thereof with a specific disorder from the extensive list of different types diseases and conditions.

Level of Skill in the Art

The level of skill in the art is deemed to be high.

Conclusion

In the instant case, as discussed above, the level of unpredictability in the association of any genomic rearrangement and any particular disease, where there is no teaching in the specification or art that any specific gene or gene variant is sufficient alone to diagnose any disease, in concert with the teaching that many published association studies are simply wrong supports a finding of undue experimentation. The specification provides the ordinary practitioner with no written description or guidance that leads to a reliable method of associating any specific differentially expressed or variant gene with any disease state. Furthermore, the specification does not provide guidance to overcome art-recognized problems in the association of mutations with diseases as shown by Lucentini, Wacholder, and Ionnadis. Finally, the quantity of experimentation is immense. Thus, given the broad claims to the diagnosis of a large

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number of pathologies based on the detection of any genomic rearrangement in an art whose nature is identified as unpredictable, the unpredictability of that art, the large quantity of research required to define these unpredictable variables, the lack of guidance provided in the specification, the absence of any working examples and the negative teachings in the prior art balanced only against the high skill level in the art, the inevitable conclusion is that it would require undue experimentation for one of skill in the art to perform the method of the claims as broadly written.

Claim Rejections - 35 USC § 112 - 1st paragraph (Written Description)

7. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 26-39 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 26-39 are directed to a multiplex amplification method utilizing composite primers claimed in terms of their thermodynamic properties (see claim 9). Specifically, the primers must include a 5' tag sequence that does not hybridize to the target nucleic acid, and furthermore, this tag must increase the melting temperature of the primer 10-15C (part d of claim 9). Also, the primers must not hybridize to themselves or other primers in the reaction mixture

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with a free energy greater than 14 kcal/mole as determined by "Primer Premier" software version 5.0 (part e of claim 9).

Applicant's specification teaches general rules for calculating free energies of hybridization based on nearest neighbor interactions (pages 19-22), but does not describe how the free energies required by claim were calculated other than to cite the aforementioned software program. Applicant neither describes the control parameters used when calculating free energies using the Primer Premier software nor presents any sort of output demonstrating that the disclosed composite primers possess the required free energies. Moreover, the Primer Premier software may change during the pendency of the application or any patent issued thereupon. For example, the algorithm used to calculate thermodynamic properties may change while the software retains the version 5.0 designation. Such changes would make it virtually impossible for an ordinary practitioner to know whether or not a particular primer pair infringed upon the instant claims. Finally, since neither the software nor the specific algorithm used to calculate the thermodynamic properties of the oligonucleotides is freely available, an ordinary practitioner would be required to purchase potentially superfluous software in order to determine if the instant claims have been infringed upon. In short, it is entirely unclear whether or not the claimed primers possess the required free energies since Applicant has not presented the appropriate data or taught one of ordinary skill how to calculate the free energies using the software. Therefore, it must be concluded that Applicant did not have possession of the claimed invention at the time of filing.

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Claim Rejections - 35 USC § 112 - 2nd paragraph

8. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 26-39 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 26-39 are indefinite, because use of the phrase "characterized in that" in claims 26-39 causes the scope of the claims to be unclear. Substitution of this phrase with language such as "comprising" or "wherein" should correct this problem.

Claims 26-39 are further indefinite, because these claims recite phrases such as "a candidate region...is selected" and "the intensity of amplification...is measured" (see steps a and d of claim 32, for example). While minute details are not required in method claims, at least the basic steps must be recited in a positive, active fashion. See <u>Ex parte Erlich</u>, 3 USPQ2d, p. 1011 (Bd. Pat. App. Int. 1986).

Claims 26-39 are further indefinite, because claim 26 requires the use of the primers defined in any of claims 9-18 in the multiplex amplification method. Claim 9 contains the trademark/trade name "Primer Premier" software. Where a trademark or trade name is used in a claim as a limitation to identify or describe a particular material or product, the claim does not comply with the requirements of 35 U.S.C. 112, second paragraph. See *Ex parte Simpson*, 218 USPQ 1020 (Bd. App. 1982). The claim scope is uncertain since the trademark or trade name cannot be used properly to identify any particular material or product. A trademark or trade name is used to identify a source of goods, and not the goods themselves. Thus, a trademark or

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trade name does not identify or describe the goods associated with the trademark or trade name. In the present case, the trademark/trade name is used to identify/describe software for calculating thermodynamic properties of primers and, accordingly, the identification/description is indefinite.

Claim 28 is further indefinite, because it recites a broad and narrow range in the same claim. A broad range or limitation together with a narrow range or limitation that falls within the broad range or limitation (in the same claim) is considered indefinite, since the resulting claim does not clearly set forth the metes and bounds of the patent protection desired. See MPEP § 2173.05(c). Note the explanation given by the Board of Patent Appeals and Interferences in *Ex parte Wu*, 10 USPQ2d 2031, 2033 (Bd. Pat. App. & Inter. 1989), as to where broad language is followed by "such as" and then narrow language. The Board stated that this can render a claim indefinite by raising a question or doubt as to whether the feature introduced by such language is (a) merely exemplary of the remainder of the claim, and therefore not required, or (b) a required feature of the claims. Note also, for example, the decisions of *Ex parte Steigewald*, 131 USPQ 74 (Bd. App. 1961); *Ex parte Hall*, 83 USPQ 38 (Bd. App. 1948); and *Ex parte Hasche*, 86 USPQ 481 (Bd. App. 1949). In the present instance, claim 28 recites the broad recitation 90 to 500 bp, and the claim also recites 90 to 300 bp, which is the narrower statement of the range/limitation.

Regarding claim 29, the phrase "such as" renders the claim indefinite because it is unclear whether the limitations following the phrase are part of the claimed invention. See MPEP § 2173.05(d).

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Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

- (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
- (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
- 10. Claims 26-33 and 35-38 are rejected under 35 U.S.C. 102(a) as being anticpated by Casilli et al. (Human Mutation (September 2002) 20: 218-226; cited on IDS).

Applicant cannot rely upon the foreign priority papers to overcome this rejection because a translation of said papers has not been made of record in accordance with 37 CFR 1.55. See MPEP § 201.15.

Regarding claim 26, Casilli teaches a method for amplifying in multiplex a plurality of target nucleotide sequences present in a nucleic acid or a mixture of nucleic acids, by hybridizations and elongations of a plurality of pairs of amplification primers, wherein the plurality of pairs of amplification primers is a plurality of pairs of sense and antisense composite primers according to claim 9 (see pages 219-220 where Casilli teaches PCR amplification using primers that meet the limitations of the instant claim 9). Specifically, the primers taught by Casilli posses the following characteristics:

(1) a hybridization segment, respectively sense or antisense, which pairs with said nucleic acid or mixture of nucleic acids, so as to constitute a sense or antisense primer for one of the

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target nucleotide sequences of the plurality targeted (page 219, "Primer Design" section; see also Table 1 for a listing of the target-specific hybridization segments)

- (2) a nucleotide tag which is attached to the 5' end of said hybridization segment, but which does not pair with said nucleic acid or mixture of nucleic acids (page 219, "Primer Design" section; see also legend of Table 1)
- (3) optionally, of a non-nucleotide component (page 219, "Primer Design" section teaches that the forward primers contain the FAM fluorophore a non-nucleotide component).

The primers taught by Casilli also possess the following characteristics:

- (4) each sense composite primer has, within said plurality, an antisense composite primer with which it forms a pair of sense and antisense composite primers whose respective hybridization segments constitute, with respect to one another, a pair of sense and antisense primers for one of said target nucleotide sequences, each one of said target nucleotide sequences of the plurality targeted thus having a pair of sense and antisense composite primers which is intended for its amplification (page 219, "Primer Design" section; see also Table 1 on page 220)
- (5) all the sense composite primers contain the same nucleotide tag and all the antisense composite primers contain in the same nucleotide, the tag of the sense composite primers being different from that of the antisense composite primers (page 219, "Primer Design" section; see also Table 1 legend on page 220,
- (6) the sequence of the tag of the sense composite primers is absent from said nucleic acid or mixture of nucleic acids, or, at the very least, is only present therein at a frequency at least two times less than that predicted statistically for a random sequence of the same length, and the sequence of the tag of the antisense composite primers is absent from said nucleic acid or

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mixture of nucleic acids, or, at the very least, is only present therein at a frequency at least two times less than that predicted statistically for a random sequence of the same length (page 219 teaches that the 5' tag sequence added to the forward and reverse primers is extremely rare),

- (7) the melting temperature of each composite primer (whether it is a sense or antisense primer) has a value 10 to 15 °C higher than that which its hybridization segment would exhibit when naked without tag (see attached printout "Exhibit A"),
- (8) each composite primer of said plurality of pairs has a sequence such that no composite primer of said plurality of pairs can form, with itself or with another composite primer of the same plurality, complete or partial base pairing for which the variation in free energy ΔG ociated with the formation of this possible pairing would be greater than 14 kcal/mol (see attached printout, "Exhibit A")

Further regarding claim 26, the attached printout "Exhibit A" only contains analysis of 4 primers (11aF, 11aR, 2F, and 2R) since this is the minimum required by the claim. Using the Oligo Analyzer 3.0 freely available from Integrated DNA Technologies, the melting temperature of each primer with and without the universal tag was calculated and found to meet the limitations of step d of claim 9. Also, the free energies of hairpin and homodimer formation were calculated for each primer and were found to satisfy the requirements of step e of claim 9. Finally, the free energy of each possible heterodimer was calculated and found to meet the limitations of step e of claim 9. Regarding the use of the Oligo Analyzer software, it is noted that the Primer Premier software, version 5.0 is not freely available. Since the PTO does not have experimental capabilities, the primers were analyzed with a web-based oligonucleotide properties calculator. Since, as discussed in greater detail above, it is not clear how the free

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energies were calculated, it is virtually impossible to reproduce the calculations done by Applicant. However, since the primers appear to inherently possess the required thermodynamic characteristics, absent any evidence to the contrary the primers taught by Casilli anticipate the instant claim. MPEP 2112 section V notes, "[T]he PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his [or her] claimed product. Whether the rejection is based on inherency' under 35 U.S.C. 102, on prima facie obviousness' under 35 U.S.C. 103, jointly or alternatively, the burden of proof is the same...[footnote omitted]." The burden of proof is similar to that required with respect to product-by-process claims. In re Fitzgerald, 619 F.2d 67, 70, 205 USPQ 594, 596 (CCPA 1980) (quoting In re Best, 562 F.2d 1252, 1255, 195 USPQ 430, 433-34 (CCPA 1977))."

Regarding claim 27, Casilli teaches amplification of 4 targets using the above amplification method (see Table 1 on page 220).

Regarding claim 28, the amplified products generated by the method of Casilli are 434 bp, 297 bp, 336 bp, and 375 bp (see Table 1), thereby anticipating the instant limitation that the amplicon sizes be 90-500 bp.

Regarding claim 29, Casilli teaches inclusion of DMSO in the multiplex amplification reaction (page 220, "PCR conditions" section, especially column 2, which teaches inclusion of DMSO for "multiplex 1").

Regarding claim 30, Casilli teaches that the amplifications of said target nucleotide sequences have exponential phase kinetics (page 220, "PCR conditions" section).

Regarding claim 31, Cassilli teaches that all the pairs of composite primers are used in equimolar concentration (page 220, "PCR conditions" section).

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Regarding claim 32, Casilli teaches a method for determining the presence or absence of at least one genomic rearrangement within a genetic material B relative to a reference genetic material A, comprising:

- (a) selecting at least one nucleotide target which constitutes a marker for the rearrangement(s) to be detected
- (b) applying the amplification method according to claim 26 to genetic material B using for each target selected, a pair of composite primers, wherein material B being considered as exhibiting the genetic rearrangement when the result of amplification of the marker target obtained from the material B, is significantly different from that which is obtained from the reference material A under identical conditions, and wherein material B being considered as not exhibiting the genetic rearrangement when the result of amplification of the marker target obtained from the material B is not significantly different from that which is obtained from the reference material A under identical conditions (see pages 221-223 where Casilli teaches application of the method described above to detection of previously known and novel rearrangements in the human BRCA1 gene. Here, Casilli teaches that rearrangements generate distinguishable amplicons compared to normal controls. See also Figures 1-3).

Regarding claim 33, Casilli teaches that the at least one genomic rearrangement is a gene rearrangement (page 223).

Regarding claim 35, Casilli teaches that genetic material B comprises at least one human gene (page 223, where Casilli analyzes the BRCA1 gene).

Regarding claim 36, Casilli teaches a method for determining at least one of the limits of one or more genomic rearrangement(s) which has (have) been detected within a genetic material

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B by comparison with a reference genetic material A (see page 223, where Casilli teaches mapping the 3' and 5' boundaries of deletions), comprising:

- (a) selecting a candidate region within which said at least one limit is potentially located (page 223, where Casilli teaches mapping the boundaries of a large heterozygous deletion)
- (b) for each rearrangement, choosing a set of nucleotide targets is chosen, among which at least one is chosen to constitute marker for this rearrangement, the other target(s) being chosen on both sides or on one or other sides of this marker target inside the candidate region chosen in step (a) so as to cover the extent of this candidate region (page 223, col. 1, paragraphs 3-4),
- (c) applying the method according to claim 26 using for each target of the chosen set, at least one pair of composite primers (page 223, col. 1, paragraphs 3-4),
- (d) measuring, for each target, the intensity of amplification thus obtained from the genetic material B and comparing it to the control intensity which is obtained for this same target under the same conditions but by applying the method of amplification to reference genetic material A, (page 223, column 1, paragraphs 3-4; see also Figure 3)
- (e) determining whether, within the chosen set of targets, at least one target is amplified with an intensity not significantly different from the control intensity, and, if this is not the case, repeating steps (a) to (e) while broadening the candidate region chosen in step (a), wherein at least one limit of the or of each one of the rearrangements within genetic material B being considered to be within a zone between: the position of the marker target for the rearrangement, and the position of the target which has been amplified with an intensity not significantly different from the control intensity or, if there are several of them, with that which is closest to the marker target, (page 223, paragraphs 3-4; see also Figure 3)

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Regarding claim 37, Casilli teaches creating a genomic rearrangement map using the results obtained from the above method (page 223 and Figure 3).

Regarding claim 38, Casilli teaches a method for identifying, and optionally isolating, at least one gene liable to be involved in a genetic disease, comprising:

- (a) conducting the method of claim 32 on a genetic material B derived from organisms exhibiting the genetic disease and a genomic material which is comparable but derived from control organisms serving as reference genomic material A, so as to detect the rearrangement(s) present in the material B relative to the material A
- (b) the gene(s) affected by the detected rearrangement(s) is (are) identified, and optionally isolated, this (these) identified and optionally isolated gene(s) corresponding to the gene(s) liable to be involved in said genetic disease (see pages 221-223; see also Figures 1 & 2).
- 11. Claims 26-28, 32, 33, and 35-38 are rejected under 35 U.S.C. 102(b) as being anticipated by Duponchel et al. (Human Mutation (2001) 17: 61-70; cited on IDS).

Regarding claim 26, Duponchel teaches a method for amplifying in multiplex a plurality of target nucleotide sequences present in a nucleic acid or a mixture of nucleic acids, by hybridizations and elongations of a plurality of pairs of amplification primers, wherein the plurality of pairs of amplification primers is a plurality of pairs of sense and antisense composite primers according to claim 9 (see pages 62-63 where Duponchel teaches PCR amplification using primers that meet the limitations of the instant claim 9). Specifically, the primers taught by Duponchel posses the following characteristics:

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- (1) a hybridization segment, respectively sense or antisense, which pairs with said nucleic acid or mixture of nucleic acids, so as to constitute a sense or antisense primer for one of the target nucleotide sequences of the plurality targeted (page 63, "Indirect Fluorescent Labeling" section; see also Table 1 for a listing of the target-specific hybridization segments)
- (2) a nucleotide tag which is attached to the 5' end of said hybridization segment, but which does not pair with said nucleic acid or mixture of nucleic acids (page 63, "Indirect Fluorescent Labeling" section; see also Table 1)
- (3) optionally, of a non-nucleotide component (page 63, "Indirect Fluorescent Labeling" section and also Table 1 which teach that the forward primers contain the FAM fluorophore a non-nucleotide component).

The primers taught by Duponchel also possess the following characteristics:

- (4) each sense composite primer has, within said plurality, an antisense composite primer with which it forms a pair of sense and antisense composite primers whose respective hybridization segments constitute, with respect to one another, a pair of sense and antisense primers for one of said target nucleotide sequences, each one of said target nucleotide sequences of the plurality targeted thus having a pair of sense and antisense composite primers which is intended for its amplification (page 63, "Indirect Fluorescent Labeling" section; see also Table 1)
- (5) all the sense composite primers contain the same nucleotide tag and all the antisense composite primers contain in the same nucleotide, the tag of the sense composite primers being different from that of the antisense composite primers (page 63, "Indirect Fluorescent Labeling" section; see also Table 1)

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- (6) the sequence of the tag of the sense composite primers is absent from said nucleic acid or mixture of nucleic acids, or, at the very least, is only present therein at a frequency at least two times less than that predicted statistically for a random sequence of the same length, and the sequence of the tag of the antisense composite primers is absent from said nucleic acid or mixture of nucleic acids, or, at the very least, is only present therein at a frequency at least two times less than that predicted statistically for a random sequence of the same length (page 63, column 1 teaches that the 5' tag sequence added to the forward and reverse primers is extremely rare),
- (7) the melting temperature of each composite primer (whether it is a sense or antisense primer) has a value 10 to 15 °C higher than that which its hybridization segment would exhibit when naked without tag (see attached printout "Exhibit B"),
- (8) each composite primer of said plurality of pairs has a sequence such that no composite primer of said plurality of pairs can form, with itself or with another composite primer of the same plurality, complete or partial base pairing for which the variation in free energy ΔG ociated with the formation of this possible pairing would be greater than 14 kcal/mol (see attached printout, "Exhibit B").

Further regarding claim 26, the attached printout "Exhibit B" only contains analysis of 4 primers (D8159ex5F, D8578ex5R, BRCA1ex5F, BRCA1ex5R) since this is the minimum required by the claim. Using the Oligo Analyzer 3.0 freely available from Integrated DNA Technologies, the melting temperature of each primer with and without the universal tag was calculated and found to meet the limitations of step d of claim 9. Also, the free energies of hairpin and homodimer formation were calculated for each primer and were found to satisfy the

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requirements of step e of claim 9. Finally, the free energy of each possible heterodimer was calculated and found to meet the limitations of step e of claim 9. Regarding the use of the Oligo Analyzer software, it is noted that the Primer Premier software, version 5.0 is not freely available. Since the PTO does not have experimental capabilities, the primers were analyzed with a web-based oligonucleotide properties calculator. Since, as discussed in greater detail above, it is not clear how the free energies were calculated, it is virtually impossible to reproduce the calculations done by Applicant. However, since the primers appear to inherently possess the required thermodynamic characteristics, absent any evidence to the contrary the primers taught by Casilli anticipate the instant claim. MPEP 2112 section V notes, "[T]he PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his [or her] claimed product. Whether the rejection is based on inherency' under 35 U.S.C. 102, on prima facie obviousness' under 35 U.S.C. 103, jointly or alternatively, the burden of proof is the same...[footnote omitted]." The burden of proof is similar to that required with respect to product-by-process claims. In re Fitzgerald, 619 F.2d 67, 70, 205 USPQ 594, 596 (CCPA 1980) (quoting In re Best, 562 F.2d 1252, 1255, 195 USPQ 430, 433-34 (CCPA 1977))."

Regarding claim 27, Duponchel teaches amplification of 6 targets using the above amplification method (see page 62, column 2 and Table 1).

Regarding claim 28, Duponchel teaches amplified products of 376 bp and 490 bp (see Table 1). Since the claims only require amplification of 2 targets in multiplex, the teachings of Duponchel meet the limitations of claim 28.

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Regarding claim 32, Duponchel teaches a method for determining the presence or absence of at least one genomic rearrangement within a genetic material B relative to a reference genetic material A, comprising:

- (a) selecting at least one nucleotide target which constitutes a marker for the rearrangement(s) to be detected
- (b) applying the amplification method according to claim 26 to genetic material B using for each target selected, a pair of composite primers, wherein material B being considered as exhibiting the genetic rearrangement when the result of amplification of the marker target obtained from the material B, is significantly different from that which is obtained from the reference material A under identical conditions, and wherein material B being considered as not exhibiting the genetic rearrangement when the result of amplification of the marker target obtained from the material B is not significantly different from that which is obtained from the reference material A under identical conditions (see pages 64-68 where Duponchel teaches application of the method described above to detection of previously known and novel rearrangements in the human C1NH gene. Here, Duponchel teaches that rearrangements generate distinguishable amplicons compared to normal controls (pages 67-68; see also Figures 1 & 2)).

Regarding claim 33, Duponchel teaches that the at least one genomic rearrangement is a gene rearrangement (page 64, column 2).

Regarding claim 35, Duponchel teaches that genetic material B comprises at least one human gene (page 64, column 1, where the human C1NH gene was analyzed).

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Regarding claim 36, Duponchel teaches a method for determining at least one of the limits of one or more genomic rearrangement(s) which has (have) been detected within a genetic material B by comparison with a reference genetic material A (see page 64, where Duponchel teaches mapping boundaries of the rearrangements occurring in exon 4), comprising:

- (a) selecting a candidate region within which said at least one limit is potentially located (page 64, column 1, where Duponchel teaches mapping the boundaries of duplications and deletions in exon 4)
- (b) for each rearrangement, choosing a set of nucleotide targets is chosen, among which at least one is chosen to constitute marker for this rearrangement, the other target(s) being chosen on both sides or on one or other sides of this marker target inside the candidate region chosen in step (a) so as to cover the extent of this candidate region (page 64, column 1),
- (c) applying the method according to claim 26 using for each target of the chosen set, at least one pair of composite primers (page 64, column 1),
- (d) measuring, for each target, the intensity of amplification thus obtained from the genetic material B and comparing it to the control intensity which is obtained for this same target under the same conditions but by applying the method of amplification to reference genetic material A, (page 64, column 1)
- (e) determining whether, within the chosen set of targets, at least one target is amplified with an intensity not significantly different from the control intensity, and, if this is not the case, repeating steps (a) to (e) while broadening the candidate region chosen in step (a), wherein at least one limit of the or of each one of the rearrangements within genetic material B being considered to be within a zone between: the position of the marker target for the rearrangement,

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and the position of the target which has been amplified with an intensity not significantly different from the control intensity or, if there are several of them, with that which is closest to the marker target, (page 64)

Regarding claim 37, Duponchel teaches creating a genomic rearrangement map using the results obtained from the above method (page 64, column 1 – column 2).

Regarding claim 38, Duponchel teaches a method for identifying, and optionally isolating, at least one gene liable to be involved in a genetic disease, comprising:

- (a) conducting the method of claim 32 on a genetic material B derived from organisms exhibiting the genetic disease and a genomic material which is comparable but derived from control organisms serving as reference genomic material A, so as to detect the rearrangement(s) present in the material B relative to the material A
- (b) the gene(s) affected by the detected rearrangement(s) is (are) identified, and optionally isolated, this (these) identified and optionally isolated gene(s) corresponding to the gene(s) liable to be involved in said genetic disease (see 64-68 and also Figures 1-2).

Claim Rejections - 35 USC § 103

- The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all 12. obviousness rejections set forth in this Office action:
 - (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

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This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

13. Claims 29-31 are rejected under 35 U.S.C. 103(a) as being unpatentable over Duponchel et al. (Human Mutation (2001) 17: 61-70; cited on IDS) in view of Varadaraj et al. (Gene (1994) 140: 1-5).

Duponchel teaches the method of claim 26, as discussed above.

Regarding claim 30, Duponchel teaches that the amplifications of said target nucleotide sequences have exponential phase kinetics (page 63-64).

Regarding claim 31, Duponchel teaches that six of the twelve primers included in the multiplex PCR reaction mixture were used at equimolar concentrations, whereas the other six primers were used at different concentrations (see page 62, column 2).

Duponchel does not teach inclusion of an agent that facilitates strand separation, such as DMSO, in the amplification reaction, nor does Duponchel teach that all primers were used at equimolar concentrations.

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Varadaraj teaches methods of improving PCR amplification of GC-rich templates (see abstract). Regarding claim 29, Varadaraj teaches that DMSO is known to improve DNA sequencing reactions by reducing inter- and intra-strand reannealing (page 3). Varadaraj also cites two instances where the inclusion of DMSO was required to obtain a detectable amplification product (pages 3-4). Varadaraj further teaches that inclusion of DMSO may improve the specificity of PCR reactions (page 4). Finally, Varadaraj concludes, "With the SF, glycerol, DMSO, and NP-40 produced the most specific product and resulted in the greatest amplification of the segment of the G+C-rich satellite DNA [sic] (page 4)."

It would have been prima facie obvious for one of ordinary skill in the art at the time of invention to include DMSO in the multiplex amplification method taught by Duponchel.

Varadaraj expressly taught that inclusion of DMSO in PCR reactions improved the specificity of the reaction and also increased the yield by reducing inter- and intra-strand reannealing (pages 3-4). An ordinary practitioner would have been motivated by these teachings of Varadaraj to include DMSO in the PCR reaction mixture in order to improve the product yield and specificity of the reaction. An ordinary practitioner would have expected a reasonable level of success in adding DMSO to the reaction mixture taught by Duponchel, because Varadaraj expressly taught useful concentrations of DMSO to be used with the AmpliTaq enzyme used in the Duponchel method (page 4, column 1). Therefore, an ordinary practitioner of the multiplex amplification method taught by Duponchel, interested in increasing the yield by reducing strand reannealing and also improving the specificity of the reaction, would have been motivated to include DMSO

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in the reaction mixture, as suggested by Varadaraj, thus resulting in the instantly claimed method.

It would also have been prima facie obvious for one of ordinary skill in the art at the time of invention to use all of the primers at equimolar concentrations. As noted in *In re Aller*, 105 USPQ 233 at 235:

More particularly, where the general conditions of a claim are disclosed in the prior art, it is not inventive to discover the optimum or workable ranges by routine experimentation.

Routine optimization is not considered inventive and no evidence has been presented that the selection of the claimed primer concentrations was other than routine or that the results should be considered unexpected in any way as compared to the closest prior art. Therefore, the method of claim 31 is prima facie obvious in view of the cited references.

14. Claim 34 is rejected under 35 U.S.C. 103(a) as being unpatentable over Duponchel et al. (Human Mutation (2001) 17: 61-70; cited on IDS) in view of Meier et al. (American Journal of Pathology (2001) 159(6): 2031-2043).

Duponchel teaches the method of claim 32, as discussed above.

Duponchel does not teach application of the method to chromosomal rearrangement.

Meier teaches a method for detecting chromosomal rearrangements comprising multiplex PCR and capillary electrophoresis (see abstract and page 2034). Meier teaches that "molecular diagnosis of B- and T-cell non-Hodgkin lymphomas are based on determination of clonality of the respective antigen receptors and detection of specific chromosomal translocations (page

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2031, column 2)." Meier further teaches that multiplex PCR assays have made detection of these translocations faster and more efficient (page 2032, column 1; see also page 2033, column 2).

It would have been prima facie obvious for one of ordinary skill in the art at the time of invention to apply the method taught by Duponchel to the detection of chromosomal rearrangements. Meier expressly taught that detection of chromosomal rearrangements was an important molecular diagnostic criterion for B- and T-cell non-Hodgkin lymphomas (page 2031). Since Meier expressly advocated detecting chromosomal rearrangements using multiplex PCR (pages 2032-2033), an ordinary practitioner would have been motivated to apply the method taught by Duponchel to the detection of chromosomal rearrangements in order to further expand the applicability of the method with a reasonable expectation of success.

Conclusion

No claims are currently allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Angela Bertagna whose telephone number is 571-272-8291. The examiner can normally be reached on M-F, 7:30 - 5.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

JEFFREY FREDMAN

PRIMARY EXAMINER

Angela Bertagna Examiner, Art Unit 1637 November 8, 2006 amb

Attachments: Exhibit A and Exhibit B

INTEGRATED DNA TECHNOLOGIES

Exhibit A

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DILUTION

RESUSPENSION

Instructions | Definitions | Feedback ' SciTools OligoAnalyzer 3.0 # Bases ANALYZE 5'-ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA CTG AGA HAIRPIN Target Type DNA ▼ SELF-DIMER Oligo Conc HETERO-DIMER Na+ Conc NCBI BLAST TM MISMATCH LNA CONVERSION DEFAULT SETTINGS CLEAR SEQUENCE ADD TO ORDER 3' MODS RESULTS **BASE NOTATION** 5' MODS INTERNAL MODS

RESULTS

SEQUENCE:

5'- ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA CTG AGA -3'

COMPLEMENT:

5'- TCT CAG TGG TGT TCA AAT CAG TCG ACT ACT AAC GGT -3'

LENGTH:

36

GC CONTENT:

44.4 %

MELT TEMP:

63.6 °C

MOLECULAR

WEIGHT:

11068.2 g/mole

EXTINCTION COEFFICIENT:

357500 L/(mole·cm)

nmole/OD₂₆₀:

2.80

μg/OD₂₆₀:

30.96

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

 $0.25 \mu M$

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when [strand1] ≥ [strand2] Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.

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IDT Y Sci	oligoAnalyzer 3.0	•					
7		Bases				ANALYZE	
5'-TGA TTT GAA CAC	CAC TGA GA	_	Target Type	DNA ₹	•	HAIRPIN	
		•	Oligo Conc	0.25	uМ	SELF-DIME	iR
·			Na ⁺ Conc			HETERO-DIM	IER .
	•			50; i	mM	NCBI BLAS	ST .
l	المراجعة المسلم المراجعة المستقلصين المستقلص المستقل المستقل المستقل المستقل المستقل المستقل المستقل المستقل ا المراجعة المستم		3'	•		TM MISMAT	сн
CLEAR SE	QUENCE ADD TO ORDE	ER	DEFAULT	SETTINGS)	LNA CONVERS	SION
RESULTS	ASE NOTATION 5' MODS	INTE	RNAL MODS	3' MODS			
RESULTS	ASE NOTATION 5' MODS	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE:		INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAG		INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT:	C CAC TGA GA -3'	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT: 5'- TCT CAG TGG TG	C CAC TGA GA -3' T TCA AAT CA -3'	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT:	C CAC TGA GA -3'	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT: 5'- TCT CAG TGG TG LENGTH:	C CAC TGA GA -3' T TCA AAT CA -3' 20	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAG COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT:	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 %	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAG COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAG COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR WEIGHT: EXTINCTION	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C 6125.0 g/mole	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR WEIGHT: EXTINCTION COEFFICIENT:	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C 6125.0 g/mole 199600 L/(mole·cm)	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAG COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR WEIGHT: EXTINCTION COEFFICIENT: nmole/OD ₂₆₀ :	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C 6125.0 g/mole 199600 L/(mole·cm) 5.01 30.69	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR WEIGHT: EXTINCTION COEFFICIENT: nmole/OD ₂₆₀ : µg/OD ₂₆₀ :	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C 6125.0 g/mole 199600 L/(mole·cm) 5.01 30.69	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION
RESULTS SEQUENCE: 5'- TGA TTT GAA CAC COMPLEMENT: 5'- TCT CAG TGG TG LENGTH: GC CONTENT: MELT TEMP: MOLECULAR WEIGHT: EXTINCTION COEFFICIENT: nmole/OD ₂₆₀ : µg/OD ₂₆₀ : MELTING TEMPERA	C CAC TGA GA -3' T TCA AAT CA -3' 20 40.0 % 51.5 °C 6125.0 g/mole 199600 L/(mole·cm) 5.01 30.69	INTE	RNAL MODS	3' MODS	DILUTION	RESUSPE	NSION

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.

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Instructions | Definitions | Feedback SciTools OligoAnalyzer 3.0 # Bases ANALYZE 5'-TCG GAT AGC TAG TCG TCC GCC TAT CAT TAC ATG TTT HATRPIN Target Type DNA SELF-DIMER Oligo Conc HETERO-DIMER Na⁺ Conc 50 mM NCBI BLAST TM MISMATCH LNA CONVERSION CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS INTERNAL MODS RESULTS BASE NOTATION 5' MODS 3' MÓDS RESULTS DILUTION RESUSPENSION SEQUENCE: 5'- TCG GAT AGC TAG TCG TCC GCC TAT CAT TAC ATG TTT -3' COMPLEMENT: 5'- AAA CAT GTA ATG ATA GGC GGA CGA CTA GCT ATC CGA -3' 36 LENGTH: 44.4 % GC CONTENT: 63.5 °C **MELT TEMP: MOLECULAR** 10992.2 g/mole **WEIGHT: EXTINCTION** 337600 L/(mole·cm) **COEFFICIENT:** nmole/OD₂₆₀: 2.96 $\mu g/OD_{260}$: 32.56

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than
 concentration of the complementary target, which is true in majority of molecular
 biology experiments. If this is not a case, concentration of the target cannot be
 ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



	nitions Feedback		
	igoAnalyzer 3.0		· '
\sim	1307 (101726) 5.0	•	
	# Bases	•	ANALYZE
5'-CCG CCT ATC ATT A	ACA TGT TT	Target Type DNA ▼	HAIRPIN
		Oligo Conc 0.25 µM	SELF-DIMER SELF-DIMER
		Na ⁺ Conc 50 mM	NCBI BLAST
		3'	TM MISMATCH
CLEAR SEQ	UENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BA	SENOTATION 5' MODS INTER	NAL MODS 3' MODS	n sa andra de de desta a mande de d
RESULTS SEQUENCE:		DILUTION	RESUSPENSION
5'- CCG CCT ATC ATT	ACA TGT TT -3'		
COMPLEMENT:	·		•
5'- AAA CAT GTA ATG	ATA GGC GG -3'		
LENGTH:	20		
GC CONTENT:	40.0 %		
MELT TEMP:	50.3 °C	·	
MOLECULAR WEIGHT:	6018.0 g/mole		
EXTINCTION COEFFICIENT:	181900 L/(mole·cm)		
nmole/OD ₂₆₀ :	5.50		
μg/OD ₂₆₀ :	33.08		
MELTING TEMPERAT	URE SETTINGS		

TARGET TYPE:

DNA

OLIGO CONC

 $0.25~\mu M$

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



1	# Ba	ises		ANALYZE
ACC GTT AGT AGT C TGG	GA CGG ACG TTG TCA TTA GTT CT	Target Ty	De DNA ▼	HAIRPIN
		! Oligo Con	0.25 µM	SELF-DIMER
		Na ⁺ Conc	-	HETERO-DIMER
			[5 <u>0</u> , mM	NCBI BLAST
		<u>▼</u>]_3'		TM MISMATCH
SULTS	SENOTATION 5' MODS	INTERNAL MODS	3' MODS	JTION RESUSPENSIO
SULTS QUENCE: ACC GTT AGT AGT (INTERNAL MODS	3' MODS	
SULTS QUENCE: ACC GTT AGT AGT (MPLEMENT:	CGA CGG ACG TTG TCA TTA GTT C	INTERNAL MODS	3' MODS	
SULTS QUENCE: ACC GTT AGT AGT OF MPLEMENT: CCA AAG AAC TAA	CGA CGG ACG TTG TCA TTA GTT C	INTERNAL MODS	3' MODS	
SULTS QUENCE: ACC GTT AGT AGT COMPLEMENT: CCA AAG AAC TAA	CGA CGG ACG TTG TCA TTA GTT COTGA CAA CGT CCG TCG ACT ACT A	INTERNAL MODS	3' MODS	
SULTS SULTS QUENCE: ACC GTT AGT AGT C MPLEMENT: CCA AAG AAC TAA NGTH: CONTENT:	CGA CGG ACG TTG TCA TTA GTT C TGA CAA CGT CCG TCG ACT ACT A 39 46.2 %	INTERNAL MODS	3' MODS	
SULTS QUENCE: ACC GTT AGT AGT COMPLEMENT:	CGA CGG ACG TTG TCA TTA GTT COTGA CAA CGT CCG TCG ACT ACT A	INTERNAL MODS	3' MODS	
ESULTS BAS SULTS QUENCE: ACC GTT AGT AGT OF MPLEMENT: CCA AAG AAC TAA NGTH: CONTENT: LT TEMP: DLECULAR EIGHT: TINCTION	TGA CAA CGT CCG TCG ACT ACT A 39 46.2 % 64.7 °C	INTERNAL MODS	3' MODS	
SULTS QUENCE: ACC GTT AGT AGT (MPLEMENT: CCA AAG AAC TAAT NGTH: CONTENT: ELT TEMP: DLECULAR	TGA CAA CGT CCG TCG ACT ACT A 39 46.2 % 64.7 °C 12034.8 g/mole	INTERNAL MODS	3' MODS	

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

Na⁺ CONC

50 mM monovalent salt

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

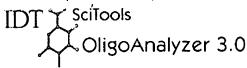
DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

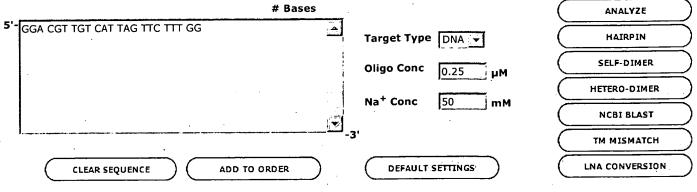
Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



Instructions | Definitions | Feedback





RESULTS

BASE NOTATION

5' MODS

INTERNAL MODS

3' MODS

DILUTION

RESUSPENSION

RESULTS

SEQUENCE:

5'- GGA CGT TGT CAT TAG TTC TTT GG -3'

COMPLEMENT:

5'- CCA AAG AAC TAA TGA CAA CGT CC -3'

LENGTH:

23

GC CONTENT:

43.5 %

MELT TEMP: MOLECULAR 54.0 °C

WEIGHT:

7091.6 g/mole

EXTINCTION

COEFFICIENT:

216700 L/(mole·cm)

nmole/OD₂₆₀:

4.61

μg/OD₂₆₀:

32.73

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
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Oligo Conc = [strand1] - [strand2]/2 when [strand1] ≥ [strand2] Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

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Instructions Definitions Feedback IDT SciTools OligoAnalyzer 3.0	
# Bases	ANALYZE
5'-TCG GAT AGC TAG TCG TAC ATG TCT TTT CTT CCC TAG TAT G Target Type DN	HAIRPIN
Oligo Conc 0.2	SELE-DIMER
	HETERO-DIMER
Na ⁺ Conc 50	MM NCBI BLAST
	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTI	INGS LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3	' MODS
RESULTS SEQUENCE:	DILUTION RESUSPENSION
5'- TCG GAT AGC TAG TCG TAC ATG TCT TTT CTT CCC TAG TAT G -3'	
COMPLEMENT: 5'- CAT ACT AGG GAA GAA AAG ACA TGT ACG ACT AGC TAT CCG A -3'	
I FNCTH: 40	

GC CONTENT:

42.5 %

MELT TEMP: MOLECULAR 62.6 °C

WEIGHT:

12234.0 g/mole

EXTINCTION COEFFICIENT:

374000 L/(mole·cm)

nmole/OD₂₆₀:

2.67

 $\mu g/OD_{260}$:

32.71

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
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γ	oligoAnalyzer 3.0					
		# Bases	•			ANALYZE
ACA TGT CTT TTC	TTC CCT AGT ATG		Target Type	DNA ₹		HAIRPIN
			Oligo Conc			SELF-DIMER
			Oligo Colic	0.25	μΜ	HETERO-DIMER
,			Na ⁺ Conc	50	mM	
		F				NCBI BLAST
			3'			TM MISMATCH
CLEAR SE	OUENCE ADD TO ORI	DER	DEFAULT	SETTINGS)	LNA CONVERSION
RESULTS	ASE NOTATION 5' MOD	S INTER	RNAL MODS	3' MODS		
. See the see of the s	ASE NOTATION 5' MOD	S INTER	RNAL MODS	3' MODS	DILUTION	RESUSPENSION
SULTS	ASE NOTATION 5' MOD	5 INTEF	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE:	TTC CCT AGT ATG -3'	5 INTER	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC	The second secon	S INTER	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC	The second secon	S INTEF	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC MPLEMENT: CAT ACT AGG GA	TTC CCT AGT ATG -3'	S INTEF	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC DMPLEMENT: CAT ACT AGG GA NGTH:	TTC CCT AGT ATG -3' A GAA AAG ACA TGT -3' 24 37.5 %	S INTEF	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC DMPLEMENT: CAT ACT AGG GA NGTH: CONTENT:	TTC CCT AGT ATG -3' A GAA AAG ACA TGT -3' 24	S INTER	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC MPLEMENT: CAT ACT AGG GA NGTH: CONTENT: ELT TEMP: DLECULAR	TTC CCT AGT ATG -3' A GAA AAG ACA TGT -3' 24 37.5 %	S INTER	RNAL MODS	3' MODS		RESUSPENSION
SULTS QUENCE: ACA TGT CTT TTC DMPLEMENT: CAT ACT AGG GA NGTH: CONTENT: ELT TEMP: DLECULAR EIGHT: CTINCTION	TTC CCT AGT ATG -3' A GAA AAG ACA TGT -3' 24 37.5 % 52.3 °C	S INTER	RNAL MODS	3' MODS		RESUSPENSION
ESULTS EQUENCE: - ACA TGT CTT TTC DMPLEMENT:	TTC CCT AGT ATG -3' A GAA AAG ACA TGT -3' 24 37.5 % 52.3 °C 7259.8 g/mole	S INTER	NAL MODS	3' MODS		RESUSPENSION

PILLITING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
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 biology experiments. If this is not a case, concentration of the target cannot be
 ignored and you should enter in the box,

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Melting temperature accuracy and models: (Oligo/Template)

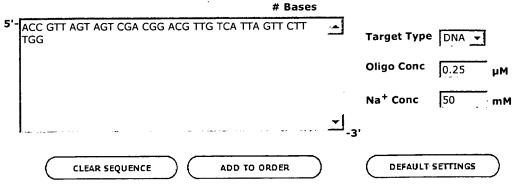
DNA/DNA: +/- 1.4°C (Allawi '97) LNA/DNA: +/- 2.0°C (McTigue '04) RNA/DNA: +/- 2.7°C (Sugimoto '95) DNA/RNA: +/- 2.7°C (Sugimoto '95) RNA/RNA: +/- 1.3°C (Xia '98)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
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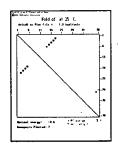


RESULTS

INTERNAL MODS

mFold Input

General Information



Sequence Name: 39 Base Oligo

Batch Date:

11/8/2006

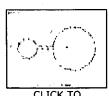
Sequence:

ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG

ADD TO ORDER

CLICK TO VIEW DOT PLOT

Structure 1



ΔG

-3.69 kcal.mole⁻¹

TM

56.2 °C

ΔН

-39.1 kcal.mole⁻¹

ΔS

-118.7 cal.K⁻¹mole⁻¹

CLICK TO **ENLARGE**

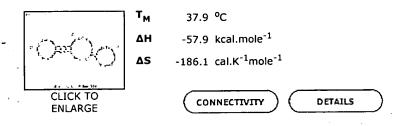
CONNECTIVITY

DETAILS

Structure 2

ΔG

-2.39 kcal.mole⁻¹



nstructions Definitions Feedback	
IDT Y SciTools	
OligoAnalyzer 3.0	
# Bases	ANALYZE
Target Type DNA ▼	HAIRPIN
Oline Cone	SELF-DIMER
Oligo Conc 0.25 µM	HETERO-DIMER
Na ⁺ Conc 50 mM	NCBI BLAST
-3'	TH MISMATCH
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	LNA CONVERSION
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	(Elin conversion
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS	•
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS	
HOMO-DIMER ANALYSIS	
Dimer Sequence 5'- ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3'	
> - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3	•
Maximum Delta G -71.89 kcal/mole	
Delta G -9.45 kcal/mole Base Pairs 6	•
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: :	
, GGIIICIIGAIIACIGIIGCAGGCAGCIGAIGAIIGCCA	**
Delta G -8.02 kcal/mole	
Base Pairs 4	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::::	•
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -6.3 kcal/mole Base Pairs 4	
•	•
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
::	

Delta G -4.95 kcal/mole Base Pairs 3
base runs 5
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA
Delta G -4.95 kcal/mole
Base Pairs 3
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: :: ::: : : :
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA
Delta G -3.61 kcal/mole
Base Pairs 2
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: :
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA
Delta G -3.61 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
] ::
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA
Delta G -3.61 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : : :: : : :
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA
Delta G -3.61 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::::::::::::::::::::::::::::::	
Delta G -2.92 kcal/mole Base Pairs 3	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::: 3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -2.92 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : ::: :: 3 · GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -2.92 kcal/mole Base Pairs 3	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : ::: : : 3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -1.95 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: : 3 · GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -1.95 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	

Delta G

Base Pairs 2

-3.61 kcal/mole

	-1.6 kcal/mole	
Base Pairs		
	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
	TTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G Base Pairs	-1.6 kcal/mole 2	
5' ACCGT	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
3' (:: GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	÷
	-1.6 kcal/mole	
Base Pairs	3 2	
5' ACCGT	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: :	
3 '	GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Base Pairs	-1.57 kcal/mole 2 TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
3'	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
	·	
Delta G Base Pairs	-1.57 kcal/mole	
2430 1 4113		
5' ACCGT	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :	
Delta G Base Pairs	-1.47 kcal/mole s 2	
5' ACCGT	TAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : : : :	
3 '	GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	

Delta G -1.34 kcal/mole Base Pairs 2

5'	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTC	TTTGG
·	::	•
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGAT	rgattgcca	
		•
Delta G -1.34 kcal/mole		
Base Pairs 2		•
-	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTG	
=		
	•	
3 GGTTTCTTGATTACTGTTGCAGGCAGCTGA	GATTGCCA	
Delta G -1.34 kcal/mole	•	
Base Pairs 2		•
S' ACCO	STTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
		•
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGA:		
	·	
		and the second s
•		
Delta G -1.34 kcal/mole		
Base Pairs 2	•	
200 (0.10)		
	ACGTTGTCATTAGTTCTTTGG	•
• •		
3' GGTTTCTTGATTACTGTTGCAGGCAGCTGA	GATTGCCA .	
•		
Delta G -1.34 kcal/mole	• •	
Base Pairs 2		
	•	
5' ACCGTTAGTAGTCC	SACGGACGTTGTCATTAGTTCTTTGG	• • • • • • • • • • • • • • • • • • •
, ACCGITAGIAGICO	::	
J GGIIICIIGAIIACIGIIGCAGGCAGCTGA	TGAT 1000A	
Dalta C 1 24 kani/masia		
Delta G -1.34 kcal/mole Base Pairs 2	•	•
pase rails 2		
5 ' ACCGTTAGTAGTCGACG	GGACGTTGTCATTAGTTCTTTGG	
·	::	· · · · · · · · · · · · · · · · · · ·
3 ' GGTTTCTTGATTACTGTTGCAGGCAGCTGA	rgattgcca ·	

Delta G -1.34 kcal/mole **Base Pairs** 2

: : : : : : : : : : : : : : : : : :	
Delta G -1.34 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::: ::::: 3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -0.96 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: : 3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	· ·
Delta G -0.96 kcal/mole Base Pairs 2	
5 ' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : 3 ' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -0.96 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : :::: 3' GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -0.96 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : :: : 3 · GGTTTCTTGATTACTGTTGCAGGCAGCTGATGATTGCCA	
Delta G -0.96 kcal/mole Base Pairs 2	

5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG

: : !! : :

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com



人人OligoAnalyzer 3.0	,	
# Bases	<u> </u>	ANALYZE
ACC GTT AGT AGT CGA CGG ACG TTG TCA TTA GTT CTT	Target Type DNA	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
	<u> </u>	HETERO-DIMER
	Na ⁺ Conc 50 mM	NCBI BLAST
La caracteristic de la car	<u>-3'</u>	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS II	NTERNAL MODS 3' MODS	
And the second s	the fact of the second	Commence of the second
econdary Sequence	3'	·
secondary Sequence - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3'		
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole		
Secondary Sequence ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3 Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole		
Gecondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole		
Secondary Sequence O - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Aaximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT		
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : :		
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : :		
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT		
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA		
Secondary Sequence - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3 - AccGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3 - AccGTTAGTAGTCGACGGACGTTGTCATTAGT - HILLING STAGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA Delta G -8.02 kcal/mole		
Gecondary Sequence S' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : : B' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA Delta G -8.02 kcal/mole		
econdary Sequence - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' laximum Delta G -71.89 kcal/mole leta G -11.04 kcal/mole lase Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : : AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA Delta G -8.02 kcal/mole lase Pairs 4 ACCGTTAGTAGTCGACGGACGTCGATGATGATGCCA	TCTTTGG	
Secondary Sequence 5' - ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3' Maximum Delta G -71.89 kcal/mole Delta G -11.04 kcal/mole Base Pairs 7 ACCGTTAGTAGTCGACGGACGTTGTCATTAGT : : B' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA Delta G -8.02 kcal/mole Base Pairs 4	TCTTTGG	

5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG

Delta G -5.02 kcal/mole

Delta G Base Pairs	-4.95 kcal/mole 3		
5' 3' AGAGTCA	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::: : : : ACCACAAGTTTAGTCAGCTGATGATTGCCA		
Delta G Base Pairs	-4.86 kcal/mole 4		· .
5' ACCGTT	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA		
Delta G Base Pairs	-3.61 kcal/mole 2		
5' 3' AGAGTC	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : ACCACAAGTTTAGTCAGCTGATGATTGCCA	·	
Delta G Base Pairs	-3.61 kcal/mole 2		·
5' 3' AGAGTO	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
Delta G Base Pairs			
5' 3' AGAGTO	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::: : : : : : ACCACAAGTTTAGTCAGCTGATGATTGCCA		

Delta G -3.61 kcal/mole

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -3.53 kcal/mole
Base Pairs 3
base rails 3
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
:
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
5 AGAGICACCACAAGIIIAGICAGCIGATIGATIGGGA
Delta G -3.53 kcal/mole
Base Pairs 3
The second of th
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -3.53 kcal/mole
Base Pairs 3
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : :: :
AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
D. H. G. 2.2 has l/mala
Delta G -3.3 kcal/mole
Base Pairs 3
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : : : : : : : : : : : : : : : :
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGCCA
Delta G -3.29 kcal/mole
Base Pairs 3
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : :: ::: :
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA

Delta G -3.17 kcal/mole

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTT			
111			
3' AGAG	GTCACCACAAGTTTAGTCAGCTGATGATTGCC	A	
•			
Delta G -3.07 kcal/mole			
Base Pairs 2			
·			,
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTT	PTCC		
	l I		
: : : :	I I		
3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGATT	IGCCA		
			•
Delta G -3.07 kcal/mole			
Base Pairs 2			•
•		•	
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCT	TTGG		
:: { :	:		
3 AGAGTCACCACAAGTTTAGTCAGCTGA	ATGATTGCCA		
		•	
Delta G -2.94 kcal/mole			
Base Pairs 3			
			•
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCT	PTGG		
: :: : : : : : : :			
3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTG	CCA		
Delta G -2.94 kcal/mole			
Base Pairs 3			
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCT	TTGG		
: : : : : : : : : : : : : : : : : :			
3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGA'			
, AGAGTCACCACAAGTTTAGTCAGCTGATGA			
			·····
Delta G -2.94 kcal/mole		•	
Base Pairs 3			
buse runs 3			
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCT	TTGG		
: :	:		
3 · AGAGTCACCA	CAAGTTTAGTCAGCTGATGATTGCCA		

5'	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTG				
5		•			
	: :::				
3' AGAGTC	ACCACAAGTTTAGTCAGCTGATGATTGCCA				•
				•	
					<u></u>
	•			•	
	•				
Delta G	-2.92 kcal/mole		•	•	•
Base Pairs	3 .				
		•			
			•		
E I ACCOMM	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG				
		•			
:	: : : : :				
3' AGA	GTCACCACAAGTTTAGTCAGCTGATGATTGCCA				•
		•	•		
Delta G	-1.95 kcal/mole				
Base Pairs	2				
5 · ACCGTT	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG				
J ACCUIT					•
	: 11				•
3 '	AGAGTCACCACAAGTTT	AGTCAGCTGATGATTGCCA			•
		·		•	
		•			
Delta G	1 OF Land (mark)				
Deita G	-1.95 kcal/mole				
Base Pairs					•
					·
Base Pairs					
Base Pairs	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG				
Base Pairs 5 ' ACCGTT	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	GATTGCCA			
Base Pairs 5 ' ACCGTT	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	GATTGCCA			
Base Pairs 5 ' ACCGTT	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	GATTGCCA			
Base Pairs 5 ' ACCGTT	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	GATTGCCA			
Base Pairs 5' ACCGTT 3'	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: AGAGTCACCACAAGTTTAGTCAGCTGAT	GATTGCCA			
Base Pairs 5' ACCGTT 3' Delta G	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: AGAGTCACCACAAGTTTAGTCAGCTGAT -1.94 kcal/mole	GATTGCCA			
Base Pairs 5' ACCGTT 3'	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: AGAGTCACCACAAGTTTAGTCAGCTGAT -1.94 kcal/mole	GATTGCCA			
Base Pairs 5' ACCGTT 3' Delta G	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: AGAGTCACCACAAGTTTAGTCAGCTGAT -1.94 kcal/mole	GATTGCCA			
Base Pairs 5 ACCGTT 3 Delta G Base Pairs	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	GATTGCCA			
Base Pairs 5 ACCGTT 3 Delta G Base Pairs	2 AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: AGAGTCACCACAAGTTTAGTCAGCTGAT -1.94 kcal/mole	GATTGCCA			
Base Pairs 5 ACCGTT 3 Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	GATTGCCA			
5' ACCGTT Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
5' ACCGTT Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
5' ACCGTT Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
5' ACCGTT Delta G Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5' ACCGTT 3' Delta G Base Pairs 5' ACCGTT 3'	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Delta G	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5' ACCGTT 3' Delta G Base Pairs 5' ACCGTT 3'	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Delta G	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::				
Base Pairs 5 ACCGTT 3 Base Pairs 5 ACCGTT 3 Base Pairs	AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ::	AGCTGATGATTGCCA			

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : :	
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.57 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
:: :: : : : 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
	·
Delta G -1.57 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: : : : : :	
3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	•
Delta G -1.57 kcal/mole	
Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	•
Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: 3	
Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
:	*

Delta G

Base Pairs 2

-1.6 kcal/mole

Base Pairs 2	
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : : : :	
3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	ı
Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole	
Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
:: 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole Base Pairs 2	•
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :	
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole Base Pairs 2	
Dase Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: ::	
3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : :: : :	
3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	

34 kcal/mole

Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : 3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : : 3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -1.34 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	
Delta G -0.96 kcal/mole Base Pairs 2	
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: : 3	
Delta G -0.96 kcal/mole Base Pairs 2	
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA	

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com



IDT SciTools OligoAnalyzer 3.0	
OligoAnalyzer 3.0	
# Bases	ANALYZE
ACC GTT AGT AGT CGA CGG ACG TTG TCA TTA GTT CTT TARGET TYPE TARGET TYPE TARGET TYPE TARGET TYPE	HAIRPIN
Olina Cara	SELF-DIMER
Oligo Conc 0.25 µM	HETERO-DIMER
Na ⁺ Conc 50 mM	NCBI BLAST
	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	LNA CONVERSION
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	
DESILITS RASE NOTATION 5' MODS INTERNAL MODS 3' MODS	
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS	
rimary Sequence	•
- ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3'	
Secondary Sequence	•
'- TCGGATAGCTAGTCGTACATGTCTTTCCTTCCCTAGTATG -3'	•
faximum Delta G -71.89 kcal/mole	
Delta G -6.68 kcal/mole	
Base Pairs 3	
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTT	TGG
GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•
	·
Delta G -6.53 kcal/mole	•
Base Pairs 4	
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : :	
GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -5.19 kcal/mole	
Base Pairs 3	

Delta G	-4.95 kcal/mole
Base Pairs	3
5'	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3 : СТАТСА	TCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
5 0111101	
Delta G	-4.95 kcal/mole
Base Pairs	3
5'	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
	: : : : : : : : : : : : : : : : : : :
	ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
3 GTATGE	MCCCTTCTTTCTGTACATGCTGATAGGCT
Delta G	-4.64 kcal/mole
Base Pairs	
Dase Falls	
5' ACCGTT	PAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3 1.0001	: :: : : : :: :
3'	GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
	\cdot
Dolta G	-3.61 kcal/mole
Base Pairs	2
r.	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
5 '	
	:
3' GTATG	ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G	-3.61 kcal/mole
Base Pairs	2
•	·
5'	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
	:: :: :: :: : : : : : : : : : : : : :
3' GTATG	ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

Delta G -3.61 kcal/mole Base Pairs 2

 ${\tt 3} \cdot {\tt GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT}$

3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.43 kcal/mole Base Pairs 3
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: : : : : : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.43 kcal/mole Base Pairs 3
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.3 kcal/mole Base Pairs 3
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :::
Delta G -3.07 kcal/mole Base Pairs 2
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.07 kcal/mole Base Pairs 2
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG

Delta G -3.07 kcal/mole Base Pairs 2

3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -2.92 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : : 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -2.92 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : : : : : :	
Delta G -2.92 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ::: : : : : : : : : : : : : : : : :	
Delta G -2.56 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -2.56 kcal/mole Base Pairs 3	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : :: 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	

5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	•
: : : : : : : : : : : : :	
Delta G -2.56 kcal/mole Base Pairs 3	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: : : : : : :	
:: : : : : : : : : : : : : : : : :	
Delta G -2.56 kcal/mole Base Pairs 3	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -2.3 kcal/mole Base Pairs 3	
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : 3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -1.95 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: : : 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: :: 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•

	•
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
•	
: : : : :	·
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
base rairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : ::	
	•
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
•	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : : : : : : : : : : : : : : : :	
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
· · · · · · · · · · · · · · · · · · ·	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
11	
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
	· · · · · · · · · · · · · · · · · · ·
Delta G -1.57 kcal/mole	
Base Pairs 2	
	·
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : :	
3 · GTATGATCCCTTCTTTCTGTACATGCTGATCGATAGGCT	

-1.6 kcal/mole

Delta G -1 Base Pairs 2

Base Pairs 2
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
:: : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
5 GIAIGAICCCITCITITCIGIACAIGCIGAIGCGI
Delta G -1.57 kcal/mole
Base Pairs 2
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
· · · · · · · · · · · · · · · · · · ·
Delta G -1.34 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -1.34 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -1.34 kcal/mole . Base Pairs 2
Dase Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : : :
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

Delta G

-1.57 kcal/mole

Delta G	-1.34 kcal/mole
Base Pairs	
5 / <u>እ</u> ሮርርጥፕ	'AGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
JACCOTT	
3 '	GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
,	GIRIOMICCOTTOTITICIO MONTOCIO MONTOCIO
Delta G	-0.96 kcal/mole
Base Pairs	
5 '	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
2.	: :
21 002002	YTCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
3. GTATGA	MCCCTTCTTTCTGTACATGCTGATCGATAGGCT
Delta G	-0.96 kcal/mole
Base Pairs	
5' ACCGTT	PAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG .
	::::
3'.	GTATGATCCCTTCŢTTTCTGTACATGCTGATCGATAGGCT
	die the Disease Analysis seetest aug Tochnical Support Croup
1-800-328-2	s regarding the Dimer Analysis contact our Technical Support Group 2661 or e-mail TechSupport@idtdna.com
	reconstruction of the contract

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# Bases ** ANALYZE ** ANALYZE ** ANALYZE ** Target Type DNA - MAIRPIN ** Oligo Conc 0.25	Instructions Definitions Feedback	i de la compania del compania de la compania de la compania del compania de la compania del compania de la compania de la compania de la compania de la compania del compania de la compania del compania de la compania de la compania de la compania del compania de la compania de la compania del compania
# Bases ANALYZE ACC GIT AGT AGT CGA CGG ACG TIG TCA TIA GIT CIT Target Type DNA HAIRPIN Oligo Conc 0.25 µM HETERO-DIMER No. ** Conc 50 mM NCSI SLAST TM MISMATCH OBFAULT SETTINGS LNA CONVERSION RESULTS BASE NOTATION 5' NOOS INTERNAL NOOS 3' HODS Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG - 3' Secondary Sequence 5' - TCGGATAGCTAGACGGACGTTGTCATTACATGTTT - 3' Maximum Delta G :71.89 kcal/mole Delta G :13.21 kcal/mole Base Pairs 6 5	IDT Y SciTools	
ACCOTTAGTAGT CGA CGG ACG TIG TCA TTA GTT CTT Target Type DNA - Oligo Conc 0.25 µM HETRO-DIMER Note Blast TM MISMATCH LINA CONVERSION RESULTS BASE NOTATION 5' MODS INTERNAL MODS 2' MODS Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGCCCCATTCATTACATCTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: :: 3' TTTGTACATTACTATCCCCCCGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3	OligoAnalyzer 3.0	
Oligo Conc		ANALYZE
Na+ Conc 50 mM HETERO-DIMER NCBI BLAST TM MISMATCH LNA CONVERSION RESULTS BASE NOTATION S' MODS INTERNAL MODS 3' MODS Primary Sequence 5'- ACCOTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Maximum Delta G :71.89 kcal/mole Base Pairs 6 5' ACCOTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : 3' TTTGTACATTACTATCCCCCTGGTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCOTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ACCOTTAGTAGTCGACGGACGTTGTCATTAGGTTCTTTGG ACCOTTAGTAGTCGACGGACGTTGTCATTAGGTTCTTTGG	5'-ACC GTT AGT AGT CGA CGG ACG TTG TCA TTA GTT CTT TGG Target Ty	ype DNA HAIRPIN
Na* Conc 50 mm HETERO-DIMER NCBI BLAST TH MISMATCH LNA CONVERSION RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGACGGACGTTGTCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGCTT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	· Oligo Cor	nc 0.25 µM
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS LINA CONVERSION RESULTS BASE ROTATION S' MODS INTERNAL MODS S' MODS Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGTCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTCG :: :: : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTCG	Not Con-	HETERO-DIMER
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS RESULTS BASE NOTATION 5' HODS INTERNAL HODS 5' HODS Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTCG :: :: : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3		
Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTCG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGACGTAGTCGATAGGCT		TM MISMATCH
Primary Sequence 5' - ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5' - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	CLEAR SEQUENCE ADD TO ORDER DEFAU	ULT SETTINGS LNA CONVERSION
Secondary Sequence 5'- TCGGATAGCTAGTCCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : :	RESULTS BASE NOTATION 5' MODS INTERNAL MODS	3' MODS
Secondary Sequence 5'- TCGGATAGCTAGCTCGCCTATCATTACATGTTT -3' Maximum Delta G -71.89 kcal/mole Delta G -13.21 kcal/mole Base Pairs 6 5' ACCGTTAGTAGCTCGACGGACGTTGCATTAGTTCTTTGG :: :: : :		
Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	5'- ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG -3' Secondary Sequence 5'- TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3'	
Base Pairs 6 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG :: :: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	Dalta C 13.21 kgal/mala	
:: :: :: : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
:: :: :: : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Delta G -6.68 kcal/mole Base Pairs 3 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
Base Pairs 3 5	:: :: :: !	
Base Pairs 3 5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	•	
III	Dase Pairs 3	
3 · TTTGTACATTACTGCCCTGCTGATCGATAGGCT	_	TGTCATTAGTTCTTTGG
	3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
		· · · · · · · · · · · · · · · · · · ·

3' TTTGTA	: : : : : : CATTACTATCCGCCTGCTGATCGATAGGCT	·
Delta G Base Pairs	-6.53 kcal/mole 4	
	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : ACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G Base Pairs	-5.19 kcal/mole 3	· .
5' 3' TTTGT	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :: ACATTACTATCCGCCTGCTGATCGATAGGCT	· .
Delta G Base Pairs	-3.61 kcal/mole	
5' 3' TTTGTA	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : ACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G Base Pairs	-3.61 kcal/mole 2	
5' 3' TTTGT	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : ACATTACTATCCGCCTGATCGATAGGCT	
Delta G Base Pairs	-3.61 kcal/mole 2	
5' 3' TTTGT	ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG ACATTACTATCCGCCTGCTGATCGATAGGCT	

Delta G -3.61 kcal/mole

5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Delta G -3.61 kcal/mole		
Base Pairs 2		
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
·		
: ::: ::: :		
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
	•	
Delta G -3.61 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
: :: : : : :		
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
J TITGIACATTACTATCCCCTCTCAMCCAMCCCT		
		•
Delta G -3.43 kcal/mole		
Base Pairs 3		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		•
	·	
Delta G -3.3 kcal/mole		
Base Pairs 3		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
: :: :		
3 '. TTTGTACATTACTATCCGCCTGATCGATAGGCT		
		
•		
Delta G -3.07 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
: ::		
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		

Delta G -3.07 kcal/mole

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
Delta G -2.56 kcal/mole			
Base Pairs 3			
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
:: ::			
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
,			
Delta G -2.56 kcal/mole	,		
Base Pairs 3			
	•		
5 ' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
: : ::			
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
Delta G -2.56 kcal/mole Base Pairs 3			
base rails 3			
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
: : : :		,	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
			_
Delta G -2.56 kcal/mole			
Base Pairs 3			
	,		
5 ' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
: : : : : : : .			
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
Delta G -2.56 kcal/mole		•	
Base Pairs 3			
	•		
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG			
: - :			
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT			

5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
:: : : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGC	CT .	
1 I I I I I I I I I I I I I I I I I I I		
	•	
Delta G -1.95 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
: : !!		
3 ' TTTGTACATTACTATCCGCCT	rgctgatcgataggct	•
Delta G -1.95 kcal/mole		•
Base Pairs 2		
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
ACCGITAGIAGICGACGGACGITGICATIAGITCITICG		
3 TTTGTACATTACTAT	CCGCCTGCTGATCGATAGGCT	
	•	
Delta G -1.6 kcal/mole		
Base Pairs 2		
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
: : : : : :	•	
3 · TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Delta G -1.6 kcal/mole		
Base Pairs 2		
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		
3 · TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Delta G -1.57 kcal/mole		
Base Pairs 2		
·		
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG		•
: :		

5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : : : : : : : : : : : : : : : :	
Delta G -1.47 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	·
5 Trigracal factatedecedecidatedatade	
Delta G -1.47 kcal/mole	,
Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: ::: : :	·
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 kcal/mole Base Pairs 2	
·	
5 ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
II :	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 kcal/mole	
Base Pairs 2	,
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG	
: : : : : : :	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : : : : : : : :	
TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	

-1.57 kcal/mole

Delta G -1 Base Pairs 2

Delta G -1.34 kcal/mole Base Pairs 2
base Falls 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: :
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT
Delta G -1.34 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT
Delta G -0.96 kcal/mole
Base Pairs 2
ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG : :
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT
Delta G -0.96 kcal/mole .
Base Pairs 2
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -0.96 kcal/mole
Base Pairs 2
•
5 · ACCGTTAGTAGTCGACGGACGTTGTCATTAGTTCTTTGG
: : :
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com



Instructions | Definitions | Feedback SciTools OligoAnalyzer 3.0 # Bases ANALYZE 5'-ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA CTG AGA Target Type DNA HAIRPIN SELF-DIMER Oligo Conc 0.25 HETERO-DIMER Na⁺ Conc mΜ NCBI BLAST TM MISMATCH LNA CONVERSION DEFAULT SETTINGS CLEAR SEQUENCE ADD TO ORDER

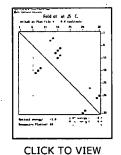
INTERNAL MODS

3' MODS

mFold Input

RESULTS

General Information



DOT PLOT

Sequence Name: 36 Base Oligo

Batch Date:

11/8/2006

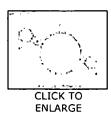
5' MODS

Sequence:

ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA

ADD TO ORDER

Structure 1



ΔG -1.06 kcal.mole⁻¹

T_M 33.0 ℃

ΔH -42.3 kcal.mole⁻¹

ΔS -138.2 cal.K⁻¹mole⁻¹

CONNECTIVITY

DETAILS



3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA

Instructions Definitions Feedback		
IDT Y SciTools		
OligoAnalyzer 3.0		
	•	
# Bases 5'-ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA CTG AGA		ANALYZE
	Target Type DNA ▼	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
	Na ⁺ Conc 50 mM	HETERO-DIMER
		NCBI BLAST
-3	, '	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	
		The state of the s
HOMO-DIMER ANALYSIS		
•		
Dimer Sequence 5'- ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3'		;
Maximum Delta G -62.48 kcal/mole		
Delta G -12.64 kcal/mole		•
Base Pairs 8		. •
		•
5 ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	J.	*
: : 3		•
Delta G -3.61 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGA(CTGATTTGAACACCACTGAGA	
: :	CIGATITGAACACCACTGAGA	
3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA		
		,
•		
Delta G -3.61 kcal/mole . Base Pairs 2		
2222.200		
5 ACCGTTAGTAGTCGACTGATTTGAAG	CACCACTGAGA	
::	•	•

Delta G -3.29 kcal/mole Base Pairs 3
5 ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : ::: 3 AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -2.94 kcal/mole Base Pairs 3
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : ::: : 3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -2.94 kcal/mole Base Pairs 3
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : :: :: :: :: :: :: :: :: :: :: :: :
Delta G -2.94 kcal/mole Base Pairs 3
5 ' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : : : : 3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.95 kcal/mole Base Pairs 2
5 ' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : ::: 3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.95 kcal/mole Base Pairs 2
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : :: : : 3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA

Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: : : : : : :
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.95 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
::
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Patha Cara 1 OF kash/mala
Delta G -1.95 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
::
3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.95 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
::
3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGCCCA
Delta G -1.94 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.94 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
:: : :: : ::
3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGCCA

Delta G

-1.95 kcal/mole ,

5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : : : : : :
3 AGAGTCACCACAAGTTTAGTCAGCTGATGCCA
Delta G -1.6 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA ::
3 · AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.57 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : :: : 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.57 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : :: : : : : : : : : : : : : : : :
Delta G -1.57 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : ::: 3' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA
Delta G -1.34 kcal/mole Base Pairs 2
5 ' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA :: 3 ' AGAGTCACCACAAGTTTAGTCAGCTGATGATTGCCA

Delta G -1.34 kcal/mole Base Pairs 2

-1.6 kcal/mole

Delta G -1 Base Pairs 2

5' AC	CCGTTAGTAGTCGACTGATTTGAACACCACTGA ::	.GA	
3 AGAGTCACCACAAGTTTAGTCAGCTGATC	•		
Delta G -1.34 kcal/mole			
Base Pairs 2			
5' ACCG	TTAGTAGTCGACTGATTTGAACACCACTGAGA		٠
 	:: :: GATTGCCA		
Delta G -1.34 kcal/mole Base Pairs 2		•	
_			
5 · ACCGTTAGTAG' :	TCGACTGATTTGAACACCACTGAGA ::::		
3 AGAGTCACCACAAGTTTAGTCAGCTGATC	GATTGCCA .		
Delta G -1.34 kcal/mole			
Base Pairs 2			
5 ACCGTTAGTAGTCGACTGATTTGAA	CACCACTGAGA	,	
: : : : : : : : : : : : : : : : : :			
J			
Delta G -1.34 kcal/mole Base Pairs 2	•		
base rails 2	•	•	
5' ACCGTTAGTAGTCGACTGATTTGAACAC			
: : : : :: 3' AGAGTCACCACAAGTTTAGTCAGCTGAT			
		•	
· · · · · · · · · · · · · · · · · · ·		,	
Delta G -1.34 kcal/mole Base Pairs 2			
5' ACCGTTAGTAGTCGACTGATTTG			
: : : : : : : : : : : : : : : : : : :	•		

Delta G -1.34 kcal/mole Base Pairs 2 .

: 3' AGAGTCACCACA	GTCGACTGATTGAACACCACTGAGA : : : : AGTTTAGTCAGCTGATGATTGCCA	
Delta G -0.96 ko Base Pairs 2	cal/mole	
5 '	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
	: :: :	
3' AGAGTCACCACA	AGTTTAGTCAGCTGATGATTGCCA	
Delta G -0.96 kg	cal/mole	
Base Pairs 2		
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
	: :	
3 ' AGAGTCACCACA	AGTTTAGTCAGCTGATGATTGCCA	
		,
	ng the Dimer Analysis contact our Technical Support Group	

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		-		
IDT Y SciTools			-	
OligoAnalyzer 3.0	0			
	# Bases		· .	
ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA	CTG AGA		· >	ANALYZE
	Targo	et Type DNA 🔻	_	HAIRPIN
	Oligo	Conc 0.25	лм <u></u>	SELF-DIMER
	Na ⁺	Conc 50	mM _	HETERO-DIMER
	©	· · · · · · · · · · · · · · · · · · ·		NCBI BLAST
	-3'			TM MISMATCH
CLEAR SEQUENCE ADD TO	ORDER E	DEFAULT SETTINGS)	LNA CONVERSION
RESULTS BASE NOTATION 5' M	IODS INTERNAL MOD	DS 3' MODS		
And the second s	The second se			A CONTRACTOR OF THE PROPERTY O
rimary Sequence				•
'- ACCGTTAGTAGTCGACTGATTTGAACACCAC	CTGAGA -3'			
econdary Sequence				
	ברכייו ביים ביים ביים ביים ביים ביים ביים ב			
TCGGATAGCTAGTCGTACATGTCTTTTCTTC	CCIAGIAIG -5			
	CCTAGIAIG 5			
' TCGGATAGCTAGTCGTACATGTCTTTTCTTC 1aximum Delta G -69.79 kcal/mole				
laximum Delta G -69.79 kcal/mole				
laximum Delta G -69.79 kcal/mole velta G -8.13 kcal/mole				
laximum Delta G -69.79 kcal/mole elta G -8.13 kcal/mole ase Pairs 5				
elta G -8.13 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA	ATTTGAACACCACTGAGA			
elta G -8.13 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : :	ATTTGAACACCACTGAGA : :	,		
elta G -8.13 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : :	ATTTGAACACCACTGAGA : :			
laximum Delta G -69.79 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : :	ATTTGAACACCACTGAGA : :			
laximum Delta G -69.79 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : : GTATGATCCCTTCTTTTCTGTACATGCTGATC	ATTTGAACACCACTGAGA : :			
laximum Delta G -69.79 kcal/mole elta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : : GTATGATCCCTTCTTTTCTGTACATGCTGATC	ATTTGAACACCACTGAGA : :			
Jaximum Delta G -69.79 kcal/mole Jelta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : : GTATGATCCCTTCTTTTCTGTACATGCTGATC Jelta G -6.68 kcal/mole Jesse Pairs 3	ATTTGAACACCACTGAGA : : CGATAGGCT	CTGATTTGAACACC	ACTGAGA ·	
Jaximum Delta G -69.79 kcal/mole Pelta G -8.13 kcal/mole Fase Pairs 5 ACCGTTAGTAGTCGACTGA : : GTATGATCCCTTCTTTTCTGTACATGCTGATC	ATTTGAACACCACTGAGA : :	CTGATTTGAACACCA	ACTGAGA	
Jaximum Delta G -69.79 kcal/mole Jelta G -8.13 kcal/mole ase Pairs 5 ACCGTTAGTAGTCGACTGA : : GTATGATCCCTTCTTTTCTGTACATGCTGATC Jelta G -6.68 kcal/mole Jesse Pairs 3	ATTTGAACACCACTGAGA : : CGATAGGCT ACCGTTAGTAGTCGAG	CTGATTTGAACACC	ACTGAGA	

ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA

Delta G -3.17 kcal/mole

5 ACCGITA	:		
3'	GTATGATCCCTTCTTTTCTGTACATG	CTGATCGATAGGCT	
		•	
Delta G	-3.07 kcal/mole		
Base Pairs		•	
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
	: : : : :: :		•
3' GTATGAT	PCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•	•
	·		
Delta G	-2.94 kcal/mole		
Base Pairs	3		
5' ACCGTTA	AGTAGTCGACTGATTTGAACACCACTGAGA		
::	: ::		
3' GTATO	GATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	·	
	•		•
	-2.94 kcal/mole		
Base Pairs	3		•
E. AGGGETT	AGTAGTCGACTGATTTGAACACCACTGAGA	·	
5 ACCGTTA	: : : : :		
3 '	GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAG	GCT	
•			
Delta G	-2.94 kcal/mole		
Base Pairs			•
			•
5' ACCGTT	AGTAGTCGACTGATTTGAACACCACTGAGA		
	111 :		•
3 '	GTATGATCCCTTCTTTTCTGTA	ACATGCTGATCGATAGGCT	
	-2.92 kcal/mole	•	
Base Pairs	3	•	
5' ACC	CGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
a. =====	: : : : :: : : ::		
J' GTATGA	TCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•	

Delta G -2.56 kcal/mole

ACCGT-TAGTAGTCGAC TGATT TGAACACCAC TGAGA	
:: · ::	
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Dalla G. 2 EC kanl/mala	
Delta G -2.56 kcal/mole Base Pairs 3	
base Pairs 3	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
: : ::	
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
The state of the s	
Delta G -2.56 kcal/mole Base Pairs 3	
base Pairs 3	
5' ACCGTTAGTAGTCGACTGAACACCACTGAGA	
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
	•
Delta G -2.56 kcal/mole	
Base Pairs 3	
5 · ACCGTTAGTAGTCGACTGAACACCACTGAGA	
:: : : : : ::	
3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
. <u> </u>	
Delta G -2.3 kcal/mole Base Pairs 3	•
Dase Falls 3	
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
: : :	
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Dolto C 1.05 kcgl/molo	
Delta G -1.95 kcal/mole Base Pairs 2	
Da3C Fall3	
5' ACCGTTAGTAGTCGACTGAACACCACTGAGA	
: :: : :: :	
3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	

5' ACCGTT.	AGTAGTCGACTGATTTGAACACCACTGAGA	
3'	: : :: : GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Dolta G	-1.95 kcal/mole	
Base Pairs		
5' ACCGTT	AGTAGTCGACTGATTTGAACACCACTGAGA	
3'	: :: GTATGATCCCTTCTTTTCTGTACATGCTGATAGGCT	
Delta G Base Pairs	-1.95 kcal/mole 2	
5' ACCGTT	AGTAGTCGACTGATTTGAACACCACTGAGA 	
Base Pairs	PAGTAGTCGACTGATTTGAACACCACTGAGA	
3'	: : : : :: :: :: GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G Base Pairs	-1.6 kcal/mole 2	
5' 3' GTATGA	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G Base Pairs	-1.6 kcal/mole 2	
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : : : : ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	

base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: : : : : : : : : : : : : : : : : :
5 GIAIGAICCCITCITITCIGIACAICCCITCCCATACCCT
Delta G -1.6 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: : : :: :: :: :: :: :: :: :: :: :: :
5 GIAIGAICCCITCITITCIGIACAIGCIGAIAGCI
Delta G -1.6 kcal/mole
Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: GTATGATCCCTTCTTTTCTGTACATGCTGATAGGCT
grandarecerrerrizeromemocor
Delta G -1.57 kcal/mole
Base Pairs 2
, , , , , , , , , , , , , , , , , , ,
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : :
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -1.57 kcal/mole Base Pairs 2
5 ' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: : : : : :
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
\cdot
The Control of the Co
Delta G -1.57 kcal/mole Base Pairs 2
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA
: : : : :
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

Delta G

-1.6 kcal/mole

Base Pairs 2					
5 ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA					. •
: : : : 3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT					
Delta G -1.57 kcal/mole Base Pairs 2					
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : :: :: :				· ·	
3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT					
	· · · · · · · · · · · · · · · · · · ·				
Delta G -1.57 kcal/mole Base Pairs 2		÷.			
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : 3 · GTATGATCCCTTCTTTTCTGTACATC	· ·	CCCT			
3 ' GTATGATCCCTTCTTTTCTGTACAT	GCIGAICGAIA	GGC1 .		-	
Delta G -1.57 kcal/mole Base Pairs 2					٠
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA			-		
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT					
Delta G -1.57 kcal/mole Base Pairs 2					
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA			•	•	
: :: : GTATGATCCCTTCTTTCTGTA	CATGCTGATCG	ATAGGCT			
Delta G -1.34 kcal/mole Base Pairs 2	***************************************				
5 · ACCGTTAGTAGTCGACTG	ATTTGAACACC	ACTGAGA			

3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

Delta G Base Pairs	-1.34 kcal/mole 2	
:	TTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : : : : ATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G Base Pairs	-1.34 kcal/mole s 2	
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
3' GTATG	: : : PATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	ar
Delta G Base Pairs	-1.34 kcal/mole s 2	
5' 3' GTATG	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : GATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G Base Pairs	-1.34 kcal/mole s 2	
5' 3' GTATO	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
Delta G Base Pairs	-1.34 kcal/mole s 2	
11	CCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : :: GATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
Delta G Base Pairs	-1.34 kcal/mole s 2	
5' ACCG	TTAGTAGTCGACTGATTTGAACACCACTGAGA	

 ${\tt GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT}$

3 '

Delta G -0.96 kcal/mole Base Pairs 2

ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA

: ||

3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

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Instructions Definitions Feedback		
IDT X SciTools		
OligoAnalyzer 3.0		
# Bases		ANALYZE
5'-ACC GTT AGT AGT CGA CTG ATT TGA ACA CCA CTG AGA	Target Type DNA ▼	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
	15.25	HETERO-DIMER
-1	* - *	NCBI BLAST
<u> </u>	3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	and the second s
Primary Sequence 5'- ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA -3'		
Secondary Sequence 5'- TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3'		
Maximum Delta G -67.39 kcal/mole		
Delta G -8.13 kcal/mole Base Pairs 5		
Sude Full 5		
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	•	
: : : : : : : : :		
3 III GIACAI IACIMI COGCIOCIO MICONIMOCI		
Delta G -6.68 kcal/mole Base Pairs 3		
5 · ACCGTTAGTAGTCG	ACTGATTTGAACACCACTGAGA	
111		
3 · TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Delta G -5.24 kcal/mole		

Delta G Base Pairs	-5.19 kcal/mole					
Dase Palls						
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA					•
	: ::					
3' TTTGTA	ACATTACTATCCGCCTGCTGATCGATAGGCT				•	
	•					
Delta G	-5 kcal/mole				•	
Base Pairs	4					•
	· .					• .
5' ACCGTT	PAGTAGTCGACTGATTTGAACACCACTGAGA					
3 '	: : : : :: ::: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT					
3	THIS INCLUDE THE CONTROL OF THE CONT					
		The state of the s				
				•		
Delta G Base Pairs	-3.61 kcal/mole 2			•		
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	•				
	H				•	
3' TTTGT	ACATTACTATCCGCCTGCTGATCGATAGGCT		•			
						
Delta G	-3.61 kcal/mole					
Base Pairs	2					
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	-				
3' TTTGT	: : : ACATTACTATCCGCCTGCTGATCGATAGGCT					
		<u> </u>		i		
Dolto G	-3.61 kcal/mole					
Base Pairs		•	•			
				•		
5' 2	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA					
3' TTTGT	ACATTACTATCCGCCTGCTGATCGATAGGCT					

Delta G -3.53 kcal/mole Base Pairs 3

5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
:: :	
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	,
•	
	•
Delta G -3.53 kcal/mole	
Base Pairs 3	
buse i direction	
5 ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
: : :	
3 · TTTGTACATTACTATCCGCCTGATCGATAGGCT	
	•
Delta G -2.92 kcal/mole	
Base Pairs 3	
base rails 3	
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	·
Delta G -2.56 kcal/mole	·
Base Pairs 3	•
buse runs 5	
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
:: ::	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
	•
Delta G -2.56 kcal/mole	
Base Pairs 3	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	·
: : ::	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
·	
Delta G -2.56 kcal/mole	•
Base Pairs 3	
buse Full's	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	

Delta G -2.3 kcal/mole

5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
$\mathbf{H}:$ $:$ $:$ $:$		
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT		
·		
Delta G -1.95 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
: : ::		
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
· · · ·		
Delta G -1.95 kcal/mole		
Base Pairs 2	* .	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	,	
: :		
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
D. H. G. A. O. F. Ive I Versale		
Delta G -1.95 kcal/mole Base Pairs 2		
base Fairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
: : TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		•
111GIACATIACIATCCGCCTGCTGATCGATAGGCT		
		•
Delta G -1.94 kcal/mole		
Base Pairs 2		
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
. : !! ::		
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Polto C 1.04 kepl/mala		
Delta G -1.94 kcal/mole Base Pairs 2		
· · · · · · · · · · · · · · · · · · ·		
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
		•
11101ACATIACIATCOCCIOCIOATCOATAGGCT		

5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA :	
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
: : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5' ACCGTTAGTAGTCGACTGAATTTGAACACCACTGAGA	
: 11	
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole	
Base Pairs 2	
5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA : : : : : :	
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.57 kcal/mole	
Base Pairs 2	•
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
: : : : :: ::	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	

Base Pairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
•		
Delta G -1.57 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
and the second of the second o		
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT		
Delta G -1.57 kcal/mole		
Base Pairs 2		
	. *	
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
Puller Communication of ST handwards	•	•
Delta G -1.57 kcal/mole Base Pairs 2	•	
base rans 2		•
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
: : :: :	•	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
		•
Delta G -1.57 kcal/mole		•
Base Pairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		•
: : :		
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		
	_	
Delta G -1.47 kcal/mole		
Base Pairs 2		
5' ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA		
: : : : :: :		
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		

-1.57 kcal/mole .

Delta G

5' ACCGTTAGTAG	TCGACTGATTTGAACACCACTGAGA : ::::	
3 '	TTTGTACATTACTATCCGCCTGATCGATAGGCT	
	·	_
5 11 6 1 34	lical/arala	
Delta G -1.34 Base Pairs 2	kcai/mole .	
5'	ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA	
_		
3' TTTGTACATTA	ACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.34	kcal/mole	
Base Pairs 2		
	$oldsymbol{\cdot}$	
	STAGTCGACTGATTTGAACACCACTGAGA	
	: : : : : ACTATCCGCCTGCTGATCGATAGGCT	
3 TIIGIACATI	CIAICCGCIGCIGAICGAIAGGCI	
Delta G -1.34 Base Pairs 2	kcai/mole	
:		
5' ACCGTTAGTAG	STCGACTGATTTGAACACCACTGAGA	
:	[: :::::	
3 ' TTTGTA	CATTACTATCCGCCTGCTGATCGATAGGCT	
•		
Delta G -1.34	kcal/mole	
Base Pairs 2		
5' ACCGTTAGTA	GTCGACTGATTTGAACACCACTGAGA	
3' .	: : : TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
3 .	111GIACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 Base Pairs 2	kcal/mole	
2430 i 4113 2		
5 ! <u>እ</u> ርርርጥሞልርጥል	GTCGACTGATTTGAACACCACTGAGA	
Jaconingin		

 ${\tt TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT}$

Delta G

۱ 3

Base Pairs 2

-1.47 kcal/mole

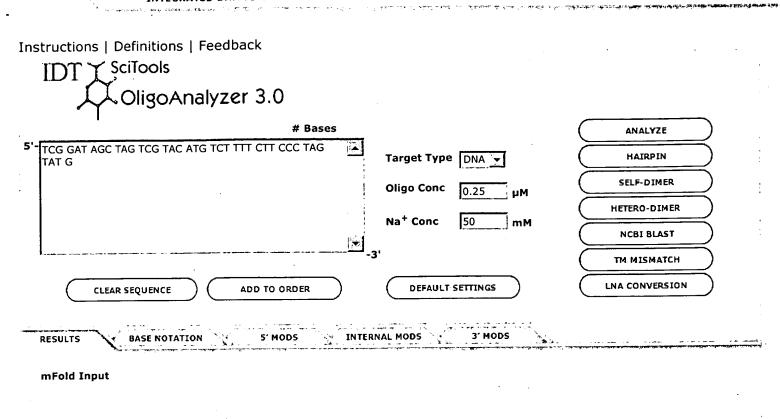
Delta G	-0.96 kcal/mole	
Base Pairs	2	

5 · ACCGTTAGTAGTCGACTGATTTGAACACCACTGAGA

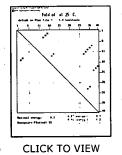
3 · TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

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Sequence Name: 40 Base Oligo 11/8/2006

Batch Date:

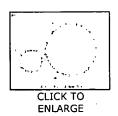
Sequence:

TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG

ADD TO ORDER

DOT PLOT

Structure 1



0.16 kcal.mole⁻¹ ΔG

T_M 22.4 °C

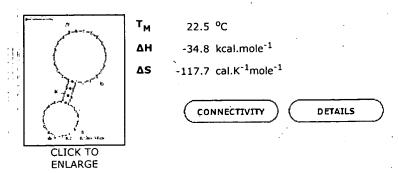
ΔН -22.7 kcal.mole⁻¹

-76.8 $cal.K^{-1}mole^{-1}$ ΔS

CONNECTIVITY DETAILS

Structure 2

ΔG 0.25 kcal.mole⁻¹



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nstructions Definitions Feedback		
IDT X SciTools		
↓↓ OligoAnalyzer 3.0		
# Bases	•	ANALYZE
TCG GAT AGC TAG TCG TAC ATG TCT TTT CTT CCC TAG	Target Type DNA 🕶	HAIRPIN
		SELF-DIMER
	Oligo Conc 0.25 µM	HETERO-DIMER
	Na ⁺ Conc 50 mM	NCBI BLAST
1.	-3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
CLEAR SEQUENCE ADD TO GROEK	OCCASE SECTION OF	
RESULTS BASE NOTATION 5' MODS INTE	ERNAL MODS 3' MODS	
	A STATE OF THE PROPERTY OF THE	And the state of t
HOMO-DIMER ANALYSIS		
Dimer Sequence 5'- TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG -3	(1	
•		
Maximum Delta G -69.79 kcal/mole		
Delta G -8.26 kcal/mole Base Pairs 6		
	CGTCTTTTCTTCCCTAGTATG	
:: :: 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•	
·		
Delta G , -8.07 kcal/mole		
Base Pairs 6		
5 · TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG	•	
: : :		
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT		
Polita G. 4 64 kgal/mala		
Delta G -4.64 kcal/mole Base Pairs 3		
5 ' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTA	ATG	
:: : : : : : : : : : : : : : :		

Delta G -4.16 kcal/mole Base Pairs 4
TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG : : : :
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -4.16 kcal/mole Base Pairs 4
5' TCGGATAGCTAGTCGTTCTTCCCTAGTATG : :::: 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -4.16 kcal/mole Base Pairs 4
5' TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG
3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.65 kcal/mole Base Pairs 4
TCGGATAGCTAGTCGTACATGTCTTTCCCCTAGTATG : : : :
: : : : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.61 kcal/mole Base Pairs 2
TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -3.61 kcal/mole Base Pairs 2
TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG : : : : :
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

Base Pairs 3			
5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
:::			
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT		•	
J			
Delta G -3.07 kcal/mole			
Base Pairs 2			
5 TCGGATAGCTAGTCGTACATGTCTTTTCCCTAGTATG			
: :: : : : : : : : :			
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			
·			
Delta G -2.56 kcal/mole	•		
Base Pairs 3			
5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
: :::::			
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			
D. D. G. 244 hard friede			
Delta G -2.44 kcal/mole Base Pairs 3			
base Pairs 5			
5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG		•	•
: ::::: : :::			
3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			
Delta G -2.3 kcal/mole			
Base Pairs 3	•		
	·		
5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
: : : : : : : : : : : : : : : :			
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			
Delta G -1.6 kcal/mole			
Base Pairs 2			
5 ' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG	•		
•			
: : : : : : : : : : : : : : : : : :			
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT			

Delta G -3.43 kcal/mole

Delta G Base Pairs	-1.6 kcal/mole 2					·	,	
	ATAGCTAGTCGTACATY : ATCCCTTCTTTTCTGTA	· :: - :						
Delta G Base Pairs	-1.6 kcal/mole 2							
5' TCGGAT	PAGCTAGTCGTACATG	PCTTTTCTTCCCTAG :: FGATCCCTTCTTTTC	•	SATCGATAGGCT	. •			
Delta G Base Pairs	-1.6 kcal/mole 2							
5' TCGGAT	PAGCTAGTCGTACATG	TCTTTTCTTCCCTAG' : :: GTATGATCCCTTC'	:	ATGCTGATCGATA	AGGCT		·	
Delta G Base Pairs	-1.57 kcal/mole 2							
5' 3'• GTATGA	· ATCCCTTCTTTTCTGT ·	. 1	:: '	GTCGTACATGTC'	PTTTCTTCCT1	AGTATG	·	
Delta G Base Pairs	-1.57 kcal/mole 2							
5'	ATCCCTTCTTTTCTGT	TCGGATAGCTAGT:: : ACATGCTGATCGATA	: :	TTTTCTTCCCTA(GTATG			
Delta G Base Pairs	-1.57 kcal/mole 2							
5' 3' GTATG		GCTAGTCGTACATGT ::::::: ACATGCTGATCGATA	:	CTAGTATG	·			

Delta G -1.57 kcal/mole Base Pairs 2

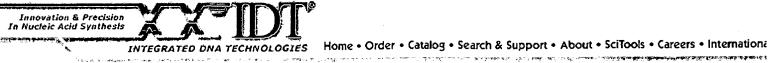
5' TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG	
: : : : : : : : : : : : : : : : : :	
Delta G -1.47 kcal/mole Base Pairs 2	
	•
TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG	
3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	•
Delta G -1.47 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	
:: 3' GTATGATCCCTTCTTTCTGTACATGCTGATCGATAGGCT	· .
Delta G -1.47 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG	
3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	·
	AND THE RESERVE OF TH
Delta G -1.34 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG	
: : :: : : : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	
•	
Delta G -0.96 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG	
: : 3' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT	

Delta G -0.96 kcal/mole

Base Pairs 2

TCGGATAGCTAGTCTTTTCTTCCCTAGTATG : :: : GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -0.96 kcal/mole Base Pairs 2
5 · TCGGATAGCTAGTCTTTTCTTCCCTAGTATG : :: : 3 · GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -0.96 kcal/mole Base Pairs 2
5 TCGGATAGCTAGTCGTACATGTCTTTCCCTAGTATG : : : : :: 3 GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT
Delta G -0.96 kcal/mole Base Pairs 2
5 TCGGATAGCTAGTCGTACATGTCTTTCTCCCTAGTATG : :: : 3
Delta G -0.96 kcal/mole Base Pairs 2
5 ' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG 3 ' GTATGATCCCTTCTTTTCTGTACATGCTGATCGATAGGCT

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com



Instructions Definitions Feedback	
IDT Y SciTools	•
OligoAnalyzer 3.0	
# Bases	ANALYZE
TCG GAT AGC TAG TCG TAC ATG TCT TTT CTT CCC TAG TAT G Target Type DNA	HAIRPIN
Oligo Conc 0.25 µM	SELF-DIMER
joint of the second of the sec	HETERO-DIMER
Na ⁺ Conc 50 mM	NCBI BLAST
-3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS	
	मान्त्र न्याप्रकारणामा वेका व्यवस्थात् कृत्योत्त्रात्वेश सम्मान्य अवस्थात् व्यवस्थात् सम्भावस्थात् वेश स्थित विद्यास्य स्थापन्ति स्थापन्ति ।
Primary Sequence 5'- TCGGATAGCTAGTCTTTTCTTCCCTAGTATG -3'	
Secondary Sequence	
5'- TCGGATAGCTAGTCCGCCTATCATTACATGTTT -3'	
Maximum Delta G -69.79 kcal/mole	
- Individual Control C	
Dalla C 0.36 land/mala	
Delta G -8.26 kcal/mole Base Pairs 6	
5 TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG	
:: ::	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
·	
Delta G -8.26 kcal/mole Base Pairs 4	
5 · TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG	
:::: : :	
3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -8.07 kcal/mole	

5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG

Base Pairs 6

3'	TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		•	,
		<u>.</u>		
D-14- C	E. C.1. kralifyrada			
Base Pairs	-5.61 kcal/mole			
5456 . 4				
_				
5 '	TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	•		
21 നനന്ന	: :: : : : ACATTACTATCCGCCTGCTGATCGATAGGCT			٠
3. 111615	SCATTACTATCCGCCTGCTGATCGATAGGCT			
			w	
Delta G	-4.64 kcal/mole			
Base Pairs	3			
•		•		
5' TCGC	SATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			•
:				
3 TTTGT	ACATTACTATCCGCCTGCTGATCGATAGGCT	•		
				•
				Was because a second and the first the first and the second and th
				•
	-4.16 kcal/mole			•
Base Pairs				
				•
5' TCGGAT	PAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG		•	
_	: :::' :			
3'	TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
Delta G	-3.61 kcal/mole			
Base Pairs				
•			•	
5'.	TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAG	TATG		
	11			
3' TTTGT	ACATTACTATCCGCCTGCTGATCGATAGGCT .			
•				
				
	-3.61 kcal/mole			•
Base Pairs	2			
	•			
5' TO	CGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG			
3' TTTGT	ACATTACTATCCGCCTGCTGATCGATAGGCT			

 $\text{IIIII.}: \quad : : : : :$

Delta G -3.43 kcal/mole Base Pairs 3

5 TCGGATAGCTAGTCGTACATGTCTTCTTCCCTAGTATG			
: : : : 3' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
Delta G -3.43 kcal/mole			•
Base Pairs 3			
5' TCGGATAGCTACATGTCTTTTCTTCCCTAGTATG			•
: :			
3 ' TTTGTACATTACTATCCGCCTGATCGATAGGCT			
Delta G -3.43 kcal/mole			•
Base Pairs 3			
5 ' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
:			
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT			
		•	
Delta G -3.14 kcal/mole			
Base Pairs 2			
5 · TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
:			
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		•	
	•		
			
Delta G -3.07 kcal/mole Base Pairs 2			
bdse Pairs 2			
5 TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG			·
: : : : : : 3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			
5 HIGHAMIACIAICCGCIGCIGAICG/MGGCI			
		•	
Delta G -3.07 kcal/mole			
Base Pairs 2			•
5 TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG			
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT			

Delta G -2.56 kcal/mole

Base Pairs 3

: : : : :	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -2.56 kcal/mole Base Pairs 3	
Dase Falls 3	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG : :	
3 · TTTGTACATTACTATCCGCCTGATCGATAGGCT	
	•
·	
Delta G -2.44 kcal/mole	
Base Pairs 3	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	•
: : :	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -2.3 kcal/mole	
Base Pairs 3	
5' TCGGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG	
: 111	
3 · TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.6 kcal/mole	
Base Pairs 2	•
5 TCGGATAGCTAGTCGTACATGTCTTTCCTTCCCTAGTATG	
: : :	
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	

5'	TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG
3 · TTTGTACATTACTATCCGCCTGCTGATC	:: GATAGGCT
Delta G -1.57 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACA : : : :: 3' TTTGTACATTACTATCCGCCTGCTGATCC	
Delta G -1.57 kcal/mole Base Pairs 2	·
5 ' TCGGATAGCTAGTCGTACATGTC' : :: : : : 3 ' TTTGTACATTACTATCCGCCTGCTGATCC	: H
Delta G -1.57 kcal/mole Base Pairs 2	
	TAGTCGTACATGTCTTTCTTCCCTAGTATG :: : GATAGGCT
Delta G -1.47 kcal/mole Base Pairs 2	
5' TCC 3' TTTGTACATTACTATCCGCCTGCTGATCC	GGATAGCTAGTCGTACATGTCTTTTCTTCCCTAGTATG GATAGGCT
Delta G -1.47 kcal/mole Base Pairs 2	
5 ' TCGGATAGCTAGTCGT: : : : 3 ' TTTGTACATTACTATCCGCCTGCTGATC	ACATGTCTTTCTTCCCTAGTATG GATAGGCT

Base Pairs 2

Base Pairs 2	
5 TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	
: : : : : : : : : : : : : : : : : :	
Delta G -1.47 kcal/mole Base Pairs 2	
5 ' TCGGATAGCTAGTCTTTTCTTCCCTAGTATG : 3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -1.47 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG : : : : . 3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 kcal/mole Base Pairs 2	
5' TCGGATAGCTACATGTCTTTTCTTCCCTAGTATG : : : : 3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -1.34 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCTTTTCTTCCCTAGTATG :: : : : : : : : : : : : : : : : : :	
Delta G -0.96 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	
: : 3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	

Delta G -1.47 kcal/mole

Base Pairs 2	•
5' TCGGATAGCTAGTCTTTTCTTCCCTAGTATG	
: : : \prod :	
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
	_
Delta G -0.96 kcal/mole	
Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCCTTCCCTAGTATG	
3 ' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
·	
Delta G -0.96 kcal/mole	
Base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCTTCCCTAGTATG	
: $:$ $:$ $:$ $:$	
3 ' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -0.96 kcal/mole Base Pairs 2	
base Pairs 2	
5' TCGGATAGCTAGTCGTACATGTCTTTCCTTCCCTAGTATG	
:: : :: : : : :	
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	
P-M-C 0.06 keel/male	
Delta G -0.96 kcal/mole Base Pairs 2	
5 TCGGATAGCTAGTCGTACATGTCTTTCCCCTAGTATG	
:	
3 · TTTGTACATTACTATCCGCCTGATCGATAGGCT	

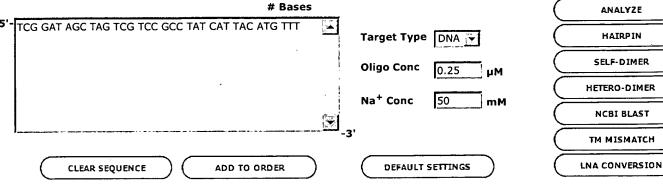
For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

Delta G

-0.96 kcal/mole

Instructions | Definitions | Feedback





RESULTS

BASE NOTATION

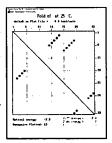
5' MODS

INTERNAL MODS

3' MOD

mFold Input

General Information



CLICK TO VIEW DOT PLOT

Sequence Name: 36 Base Oligo

Batch Date:

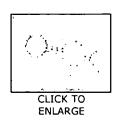
11/8/2006

Sequence:

TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT

ADD TO ORDER

Structure 1



ΔG -2.31 kcal.mole⁻¹

T_M 37.7 ℃

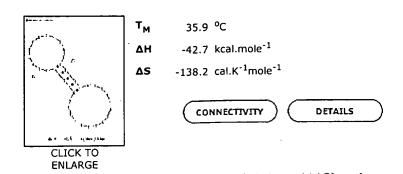
ΔH -56.4 kcal.mole⁻¹

ΔS -181.5 cal.K⁻¹mole⁻¹

CONNECTIVITY)

DETAILS

Structure 2





5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT

structions Definitions Feedback	ente may mayor separa e e a a constituir a constituir de l'acceptable de l'acceptable de l'acceptable de l'acc			
TDT Y SciTools	•			
OligoAnalyzer 3.0				
1				\
# Bases TCG GAT AGC TAG TCG TCC GCC TAT CAT TAC ATG TTT	Ţ	(ANALYZE)
and the fee fee dee this ent the first the see	Target Type DNA ▼	(HAIRPIN)
	Oligo Conc 0.25	ım (SELF-DIMER)
	Na ⁺ Conc 50	nM (HETERO-DIMER)
: ∵	· · · · · · · · · · · · · · · · · · ·	(NCBI BLAST)
	-3'	(ти мізматсн)
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS) (LNA CONVERSION)
mer Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3'			·	
mer Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' eximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole				
mer Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole se Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT	·CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole se Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: ::	CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3 ' ximum Delta G -67.39 kcal/mole ta G -8.26 kcal/mole se Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: ::	°CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole se Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: ::	CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole ta G -8.26 kcal/mole ge Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: :: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole ta G -8.26 kcal/mole ge Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: :: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	CATTACATGTTT			
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole Se Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: :: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT Ita G -8.26 kcal/mole se Pairs 4				
ner Sequence - TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT -3' ximum Delta G -67.39 kcal/mole Ita G -8.26 kcal/mole See Pairs 6 TCGGATAGCTAGTCGTCCGCCTAT :: :: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT				
TCGGATAGCTAGTCGTCCGCCTAT :: :: TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT elta G -8.26 kcal/mole use Pairs 4 TCGGATAGCTAGTCGTCCGCCTATCATT				

 ${\tt TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT}$

Base Pairs 5	•
5 TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT : :: : ::::: 3 TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -3.61 kcal/mole Base Pairs 2	
5 · TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT 3 · TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -3.61 kcal/mole Base Pairs 2	
5 · TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT :::::: ::::::::::::::::::::::::::	
Delta G -3.61 kcal/mole Base Pairs 2	
5 TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT :: : : :: 3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	
Delta G -3.43 kcal/mole Base Pairs 3	
5 ' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT : ::::: 3 ' TTTGTACATTACTATCCGCCTGATCGATAGGCT	
Delta G -3.14 kcal/mole Base Pairs 2	
5 ' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT : :: : 3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT	

- -- -

5 TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -3.07 kcal/mole
Base Pairs 2
TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
: ::::::::::::::::::::::::::::::::::
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT
Politic Control of Table Mendo
Delta G -1.57 kcal/mole Base Pairs 2
5 · TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
3 TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -1.57 kcal/mole Base Pairs 2
5 TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
::
3' TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
.
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
: : : : : :
3 TTTGTACATTACTGCCTGCTGATCGATAGGCT

Delta G

Base Pairs 2

-3.14 kcal/mole

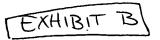
Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
: : : : : : : : : : : : : : : : : :
Palla C. 1.47 kash/mala
Delta G -1.47 kcal/mole Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
3 ' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
: : : : : : TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -1.47 kcal/mole Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
11 ::
3 · TTTGTACATTACTATCCGCCTGATCGATAGGCT
Delta G -1.34 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
:: : :: :: :: : : : : : : : : : : :
Delta G -1.34 kcal/mole Base Pairs 2
5' TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT
: :: :: :
3 TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT

Delta G -0.96 kcal/mole Base Pairs 2

-1.47 kcal/mole

Delta G

TCGGATAGCTAGTCGTCCGCCTATCATTACATGT					
' TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT		•			
elta G -0.96 kcal/mole				•	
ase Pairs 2					
TCGGATAGCTAGTCCGCCTATCATTACATGTTT					
: : : : : : : : : : : : : : : : : :					
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elta G -0.96 kcal/mole ase Pairs 2					
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: :: :					
TTTGTACATTACTATCCGCCTGATCGATAGGCT			÷		
elta G -0.96 kcal/mole					*
ase Pairs 2					
TCGGATAGCTAGTCGTCCGCCTATCATTACATGTTT					
: :				•	
TTTGTACATTACTATCCGCCTGCTGATCGATAGGCT			•		
	•		•		
					.,
or questions regarding the Dimer Analysis contact our Technical Support Group				•	



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Instructions Defir						e , a comprehensive com	
	goAnalyzer 3.0			• •			
.		# Bases				ANALYZE	
5'-TAG TCG ACG ACC G	TT AGG GTT TAC CTT CTT T	GG GCC	Target Type	DNA 「▼	\vdash	HAIRPIN	\preceq
			Oligo Conc			SELF-DIMER	5
			•	0.25 μ M		HETERO-DIMER	\vec{a}
		-1	Na ⁺ Conc	50 mM		NCBI BLAST	5
1			3'			TM MISMATCH	$\bar{\mathcal{D}}$
CLEAR SEQU	JENCE ADD TO OF	RDER	DEFAULT	SETTINGS		LNA CONVERSION	$\bar{\bigcirc}$
-				as so anno officio someonico nella disconomica nel			
RESULTS BAS	E NOTATION 5' MOI	S INTER	NAL MODS	3' MODS		Commence of the second	
RESULTS			÷	DILL	JTION)	RESUSPENSION	.).
SEQUENCE:				Unit of the control o) IION	. KESUSPERSION	9
5'- TÁG TCG ACG ACC	GTT AGG GTT TAC CTT CTT 1	rgg GCC -3'	•				
COMPLEMENT:							
5'- GGC CCA AAG AAG	GTA AAC CCT AAC GGT CGT	CGA CTA -3'					
LENGTH:	36						
GC CONTENT:	52.8 %						
MELT TEMP:	66.6 °C						
MOLECULAR WEIGHT:	11049.2 g/mole						
EXTINCTION COEFFICIENT:	331700 L/(mole·cm)						
nmole/OD ₂₆₀ :	3.01				•		
μg/OD ₂₆₀ :	33.31				i.		
MELTING TEMPERATE	IRE SETTINGS						
TARGET TYPE:	DNA						
OLIGO CONC	0.25 μΜ	•					
Na ⁺ CONC	50 mM monovalent salt						•

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than
 concentration of the complementary target, which is true in majority of molecular
 biology experiments. If this is not a case, concentration of the target cannot be
 ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



I	# Bases	· •	ANALYZE
G TIT ACC TIC TIT GGG CC		Target Type DNA	HAIRPIN
		Oligo Conc 0.25 µM	SELF-DIMER
			HETERO-DIMER
	~ !	** = = · · · · = 4	NCBI BLAST
e e comenciar e la composición de la composición dela composición de la composición dela composición de la composición d		J _{-3'}	TM MISMATCH
CLEAR SEQUENCE A	DD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
CLEAR SEQUENCE A			LNA CUNVERSION

COMPLEMENT:

5'- GGC CCA AAG AAG GTA AAC CC -3'

LENGTH:

20

GC CONTENT:

55.0 %

MELT TEMP: MOLECULAR 56.2 °C

WEIGHT:

WEIGHT: EXTINCTION 6106.0 g/mole

COEFFICIENT:

175300 L/(mole·cm)

nmole/OD₂₆₀:

5.70

 $\mu g/OD_{260}$:

34.83

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.

DILUTION

RESUSPENSION



OligoAnal	yzer 3.0					
	# Base	s				ANALYZE
CG GAT AGC TAG TCG TTG GGC	TTT GAA GCC AGG AG	<u></u>	Target Type	DNA 🔻	Č	HAIRPIN
			Oligo Conc	0.25 µM		SELF-DIMER
		. ;	N-+ C			HETERO-DIMER
	•		Na ⁺ Conc	50 mM		NCBI BLAST
			, ,			ти мізматсн
CLEAR SEQUENCE (ADD TO ORDER)	DEFAULT	SETTINGS		LNA CONVERSION

RESULTS

SEQUENCE:

5'- TCG GAT AGC TAG TCG TTG GGC TTT GAA GCC AGG AG -3'

COMPLEMENT:

5'- CTC CTG GCT TCA AAG CCC AAC GAC TAG CTA TCC GA -3'

LENGTH:

GC CONTENT:

54.3 %

MELT TEMP:

67.0 °C

MOLECULAR

WEIGHT:

10883.1 g/mole

EXTINCTION

COEFFICIENT:

340000 L/(mole·cm)

nmole/OD₂₆₀:

2.94

μg/OD₂₆₀:

32.01

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when [strand1] ≥ [strand2] Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



Instructions Defini	\cdot	
	goAnalyzer 3.0	. :
	# Bases ANALYZE	
5'-TGG GCT TTG AAG CC	CA GGA G Target Type DNA THAIRPIN	
	Oligo Conc 0.25 µM SELF-DIMER	
	HETERO-DIMER	
	Na ⁺ Conc 50 mM NCBI BLAST	!
1	-3' TM MISMATCH	
CLEAR SEQUE	TENCE ADD TO ORDER DEFAULT SETTINGS LNA CONVERSION	
RESULTS BASE	ENOTATION 5' MODS INTERNAL MODS 3' MODS	lean Tourist d'Arben de
RESULTS	DILUTION RESUSPENSION	
SEQUENCE:		
5'- TGG GCT TTG AAG C	CCA GGA G -3'	
COMPLEMENT:		
5'- CTC CTG GCT TCA AA		
LENGTH:	19	
GC CONTENT:	57.9 %	
MELT TEMP:	57.8 °C	
MOLECULAR WEIGHT:	5908.9 g/mole	:
EXTINCTION COEFFICIENT:	185000 L/(mole·cm)	
nmole/OD ₂₆₀ :	5.41	

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

31.94

OLIGO CONC

μg/OD₂₆₀:

 $0.25 \mu M$

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

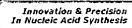
- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



INTEGRATED DNA TECHNOLOGIES

Instructions Defini			
IDT Y Scito	Ols		
A Olig	30Analyzer 3.0		
•	# Bases		ANALYZE
TAG TCG ACG ACC GT	T ACA GCA TCC AAA AAC AAT TAG G	Target Type DNA ▼	HAIRPIN
	•	Oligo Conc 0.25 µM	SELF-DIMER
		Na ⁺ Conc 50 mM	HETERO-DIMER
	<u></u>	• • • • • • • • • • • • • • • • • • •	NCBI BLAST
		3'	TM MISMATCH
CLEAR SEQUE	ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE	NOTATION 5' MODS INTER	RNAL MODS 3' MODS	and a supply of the supply of
RESULTS		DILUTIO	RESUSPENSION
SEQUENCE:			
5'- TAG TCG ACG ACC G	TT ACA GCA TCC AAA AAC AAT TAG G -3'		•
COMPLEMENT:	0 170 CTO T11 000 T00 T00 ACT A 31		
-	G ATG CTG TAA CGG TCG TCG ACT A -3' 37	•	
LENGTH: GC CONTENT:	43.2 %		•
MELT TEMP:	63.3 °C		
MOLECULAR WEIGHT:	11359.4 g/mole		
EXTINCTION COEFFICIENT:	372800 L/(mole·cm)		
nmole/OD ₂₆₀ :	2.68		
μg/OD ₂₆₀ :	30.47		

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than
 concentration of the complementary target, which is true in majority of molecular
 biology experiments. If this is not a case, concentration of the target cannot be
 ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when [strand1] ≥ [strand2] Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)-

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



	initions Feedback		
	ligoAnalyzer 3.0		
ı	# Bas	es	ANALYZE
5'-CAG CAT CCA AAA	ACA ATT AGG	Target Type DNA 🔻	HAIRPIN
			SELF-DIMER
		Oligo Conc 0.25 µM	HETERO-DIMER
		Na ⁺ Conc 50 mM	
		→ _3'	NCBI BLAST
		-3	TM MISMATCH
CLEAR SEC	QUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BA	ASE NOTATION 5' MODS	INTERNAL MODS 3' MODS	
RESULTS		DILUTIO	RESUSPENSION
SEQUENCE:	ACA ATT ACC. 31		
5'- CAG CAT CCA AAA COMPLEMENT:	ACA ATT AGG -3		
5'- CCT AAT TGT TTT	TGG ATG CTG -3'		
LENGTH:	21		
GC CONTENT:	38.1 %		
MELT TEMP: MOLECULAR WEIGHT:	50.1 °C 6416.3 g/mole		
EXTINCTION COEFFICIENT:	216100 L/(mole·cm)		•
nmole/OD ₂₆₀ :	4.63		
μg/OD ₂₆₀ :	29.69		
MELTING TEMPERAT	URE SETTINGS		
TARGET TYPE:	DNA		
OLIGO CONC	0.25 μM		

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

50 mM monovalent salt

Na⁺ CONC

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than
 concentration of the complementary target, which is true in majority of molecular
 biology experiments. If this is not a case, concentration of the target cannot be
 ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: \pm - 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



Instructions | Definitions | Feedback

IDT X SciTools	
OligoAnalyzer	3.0

# Bases	ANALYZE
TCG GAT AGC TAG TCG TGA ATG GTT TTA TAG GAA CGC TA Target Type DNA T	HAIRPIN
Oligo Conc 0.25 µM	SELF-DIMER
	HETERO-DIMER
Na ⁺ Conc 50 mM	NCBI BLAST
-31	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS	LNA CONVERSION

INTERNAL MODS

3' MODS

DILUTION

RESUSPENSION

RESULTS

RESULTS

SEQUENCE:

5'- TCG GAT AGC TAG TCG TGA ATG GTT TTA TAG GAA CGC TA -3'

5'- TAG CGT TCC TAT AAA ACC ATT CAC GAC TAG CTÁ TCC GA -3'

LENGTH:

GC CONTENT:

42.1 %

MELT TEMP:

63.0 °C

MOLECULAR

WEIGHT:

11787.7 g/mole

EXTINCTION COEFFICIENT:

379400 L/(mole·cm)

nmole/OD₂₆₀:

2.64

μg/OD₂₆₀:

31.07

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

 $0.25 \mu M$

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.

5' MODS

Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

> Oligo Conc = [strand1] - [strand2]/2 when $[strand1] \ge [strand2]$ Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.



Instructions | Definitions | Feedback SciTools OligoAnalyzer 3.0 # Bases ANALYZE GAA TGG TTT TAT AGG AAC GCT A Target Type DNA → HAIRPIN SELF-DIMER Oligo Conc HETERO-DIMER Na⁺ Conc mM NCBI BLAST TH MISMATCH LNA CONVERSION **CLEAR SEQUENCE** ADD TO ORDER DEFAULT SETTINGS RESULTS **BASE NOTATION** 5' MODS INTERNAL MODS 3' MODS **RESULTS** RESUSPENSION **DILUTION SEQUENCE:**

5'- GAA TGG TTT TAT AGG AAC GCT A -3'

COMPLEMENT:

5'- TAG CGT TCC TAT AAA ACC ATT C -3'

LENGTH:

22

GC CONTENT:

36.4 %

MELT TEMP:

50.3 °C

MOLECULAR WEIGHT:

6813.5 g/mole

EXTINCTION

COEFFICIENT:

225000 L/(mole·cm)

nmole/OD₂₆₀:

4.44

μg/OD₂₆₀:

30.28

MELTING TEMPERATURE SETTINGS

TARGET TYPE:

DNA

OLIGO CONC

0.25 µM

Na⁺ CONC

50 mM monovalent salt

MELTING TEMPERATURE ASSUMPTIONS AND LIMITATIONS

- Predictions are accurate for oligos from 8 to 60 bases in length, in neutral buffered solutions (pH 7 - 8) with monovalent cation concentrations from 10mM to 1.2 M.
- Oligo concentration is assumed to be significantly larger (at least 6x) than concentration of the complementary target, which is true in majority of molecular biology experiments. If this is not a case, concentration of the target cannot be ignored and you should enter in the box,

Oligo Conc = [strand1] - [strand2]/2 when [strand1] ≥ [strand2] Oligo Conc = ([strand1] + [strand2])/4 when [strand1] = [strand2]

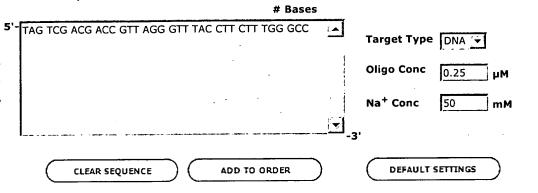
• Melting temperature accuracy and models: (Oligo/Template)

Monovalent cation correction: +/- 2.0°C (Owczarzy '04)

- Non-consecutive LNA bases hybridized to a DNA template use a model from McTigue '04. Consecutive LNA bases on a DNA template and any LNA bases on an RNA template assume RNA energetic parameters and predictions are therefore less accurate.
- Effects of chemical modifications are neglected except when the modification contains a base, e.g., 5-Methyl dC, Internal Fluorescein dT. Energetic effects of these modifications are only approximated.
- This OligoAnalyzer version does not account for effects of divalent cations.

Instructions | Definitions | Feedback







RESULTS

BASE NOTATION

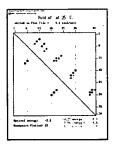
5' MODS

INTERNAL MODS

3' MODS

mFold Input

General Information



Sequence Name: 36 Base Oligo

Batch Date:

11/8/2006

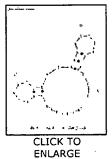
Sequence:

TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

ADD TO ORDER

CLICK TO VIEW DOT PLOT

Structure 1



ΔG -2.28 kcal.mole⁻¹

T_M 40.2 ℃

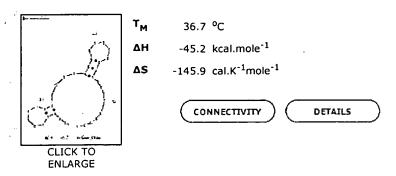
ΔH -47.5 kcal.mole⁻¹

ΔS -151.6 cal.K⁻¹mole⁻¹

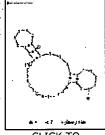
. (CONNECTIVITY

DETAILS

Structure 2







CLICK TO ENLARGE ΔG -1.66 kcal.mole⁻¹

T_M 37.7 ℃

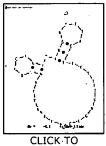
ΔH -41.7 kcal.mole⁻¹

ΔS -134.2 cal.K⁻¹mole⁻¹

CONNECTIVITY

DETAILS

Structure 4



CLICK-TO ENLARGE ΔG -1.15 kcal.mole⁻¹

T_M 33.7 °C

ΔH -38.8 kcal.mole⁻¹

ΔS -126.4 cal.K⁻¹mole⁻¹

CONNECTIVITY

DETAILS

Instructions Definitions Feedback	· · · · · · · · · · · · · · · · ·	
IDT SciTools		
OligoAnalyzer 3.0		
# Bases		ANALYZE
5'-TAG TCG ACG ACC GTT AGG GTT TAC CTT CTT TGG GCC	Target Type DNA	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
	Na ⁺ Conc 50 mM	HETERO-DIMER
<u> </u>	Equation is the control of	NCBI BLAST
	3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	Marie and the second se
HOMO-DIMER ANALYSIS		
Dimer Sequence 5'- TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC -3'		
1		
Maximum Delta G -72.71 kcal/mole		
Delta G -9.45 kcal/mole		
Base Pairs 6		
TAGTCGACGACCGTTAGGG' : :	TTTACCTTCTTTGGGCC	
3' CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT		•
Delta G -9.28 kcal/mole		
Base Pairs 4		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
. 1111		
3 · CCGGGTTTCTTCC.	ATTTGGGATTGCCAGCAGCTGAT	
	·	
Delta G -6.53 kcal/mole		
Base Pairs 4		

 ${\tt TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC}$

1111 ::::

3' CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT

5 '

Delta G -4.95 kcal/mole	•		-	
Base Pairs 3				
E	rcgacgaccgttagggtttaccttc	ምምምርርርርር ·		
5 TAG		TTTGGGCC ,		
3 · CCGGGTTTCTTCCATTTGGC				
Delta G -4.67 kcal/mole Base Pairs 3				
				•
5' TAGTCGACGACCGTTAGGG	ኮጥጥል CCጥጥCጥጥጥናGGGCC			
::				
	TTTGGGATTGCCAGCAGCTGAT			
				•
Delta G -4.41 kcal/mole				
Base Pairs 3				
•				
5' TAGTCGACGACCO	GTTAGGGTTTACCTTCTTTGGGCC			
-	: : ::: :	•		
3' CCGGGTTTCTTCCATTTGG	GATTGCCAGCAGCTGAT			•
		•		
Delta G -4.41 kcal/mole	•	•		
Base Pairs 3				
	•			
5' TAGTCGACGACCGTTAGGG	TTTACCTTCTTTGGGCC			
	:::::::::::::::::::::::::::::::::::::::			
3 ' CCGGGTTTCTTCC	ATTTGGGATTGCCAGCAGCTGAT	•		•
		•		
1		•		
Delta G -3.61 kcal/mole	•			
Base Pairs 2				
5'	TAGTCGACGACCGTTAGGGTTTAC	CTTCTTTGGGCC		
	:: : : ::			
3' CCGGGTTTCTTCCATTTGG	GATTGCCAGCAGCTGAT			
				<u> </u>
Delta G -3.61 kcal/mole				
Base Pairs 2	•	•		
		•		
5'	TAGTCGACGACCGTTAGGGTTTACC	TTCTTTGGGCC		
	::			
3 ' CCGGGTTTCTTCCATTTGG	GATTGCCAGCAGCTGAT			

	•
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : :	
3' CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT	•
Delta G -3.07 kcal/mole Base Pairs 2	·
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: : :: : : : : : : : : : : : : : :	
3 CCGGGIIICIICCAIIIGGGAIIGCCAGCAGCIGAI	
Delta G -3.07 kcal/mole	
Base Pairs 2	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : : : : : : : : : : : : : : :	
3 · CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT	
Delta G -3.07 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	- -
H ::	
3 · CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT	
P. M. G. 2071 cellusels	
Delta G -3.07 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: :: :: :: :: :: :: :: :: :: :: :: ::	
Delta G -3.07 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::	
3 · CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT	

Delta G -3.61 kcal/mole

Dase Pairs	2
E. macmoo	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
5 TAGTCG	
3'	CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT
Delta G	-3.07 kcal/mole
Base Pairs	
5' TAGTCO	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
3'	CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT
•	
Delta G	-3.07 kcal/mole
Base Pairs	2
5' TAGTCO	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
3 '	:: CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT
3	
Delta G Base Pairs	-1.6 kcal/mole 2
5'	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
	: : : : ::
3' CCGGGT	TTCTTCCATTTGGGATTGCCAGCAGCTGAT
Delta G	-1.6 kcal/mole
Base Pairs	2
5'	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
3 ' CCGGGT	: :::::::::::::::::::::::::::::::::
	
Dollar C	-1.57 kcal/mole
Base Pairs	
5' TAC	STCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
3' CCGGG	TTCTTCCATTTGGGATTGCCAGCAGCTGAT

Delta G -1.57 kcal/mole Base Pairs 2

Delta G

-3.07 kcal/mole

5 TAGTCGACCGCTTAGGTTTACCTTCTTTGGGCC :: :: : :: :: :: :: :: :: :: :: :: :		
Delta G -1.34 kcal/mole Base Pairs 2		
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: : :: :: 3 · CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT	-	
Delta G -1.34 kcal/mole Base Pairs 2		
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: :: :: 3 · CCGGGTTTCTTCCATTTGGGATTGCCAGCAGCTGAT		
Delta G -0.96 kcal/mole Base Pairs 2		
TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC 3		
Delta G -0.96 kcal/mole Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::::::::::::::::::::::::::		

For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

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Instructions | Definitions | Feedback

IDT X SciTools	
OligoAnalyzer	3.0

	# Bases	ANALYZE
; ' .	TAG TCG ACG ACC GTT AGG GTT TAC CTT CTT TGG GCC Target Type DNA -	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
		HETERO-DIMER
	Na Conc 50 mM	NCBI BLAST
		TM MISMATCH
	CLEAR SEQUENCE: ADD TO ORDER DEFAULT SETTINGS	LNA CONVERSION

RESULTS

BASE NOTATION

5' MODS

INTERNAL MODS

3' MODS

Primary Sequence

5'- TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC -3'

Secondary Sequence

5'- TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGC -3'

Maximum Delta G -72.71 kcal/mole

Delta G -9.45 kcal/mole

Base Pairs 6

TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

: |||||| :

3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT

Delta G -8.91 kcal/mole

Base Pairs 5

5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

3 · CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT

Delta G -6.53 kcal/mole

3' CGATTA	AACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G Base Pairs	-5.23 kcal/mole 4		
5' TAGTCO	GACGACCGTTAGGGTTTACCTTCTTTGGGCC : : :: : CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G Base Pairs	-4.95 kcal/mole 3		
5' 3' CGATTA	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::: AACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G Base Pairs	-4.41 kcal/mole		·
5' 3' CGATTA	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : : : : AACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G Base Pairs	-3.9 kcal/mole 3		
5' TAGTCO	GACGACCGTTAGGGTTTACCTTCTTTGGGCC : CGATTAACAAAAACCTACGACATTGCCAGCAGCTG	AT	
Delta G Base Pairs	-3.89 kcal/mole 3		
5' TAGTCO	GACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : :: : CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		

|||| ::::

Delta G -3.89 kcal/mole Base Pairs 3

5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC .
3 ' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G -3.89 kcal/mole
Base Pairs 3
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
:: : ::
3 ' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G -3.89 kcal/mole
Base Pairs 3
5 - maggaega (6) 00 00 mm
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
:: : CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G -3.61 kcal/mole
Base Pairs 2
base rails 2
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
3 ' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G -3.61 kcal/mole
Base Pairs 2
5 ' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G -3.61 kcal/mole
Base Pairs 2
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
: : : :
: : : : 3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT

Delta G -3.29 kcal/mole

_	ICGACCGTTAGGGTTTACCTTCTTTGGGCC
3' CC	ATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G	-3.14 kcal/mole
Base Pairs	2
5' TAGTCGA	CGACCGTTAGGGTTTACCTTCTTTGGGCC
	: ::::
3 '	CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
D-4- C	-3.14 kcal/mole
Base Pairs	
Base Pairs	2
5' TAGTOGA	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
3 11.0100.	
2.	CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
3 '	CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G	-3.07 kcal/mole
Base Pairs	2
5 '	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
	: :::: : :
3' CGATTA	ACAAAAACCTACGACATTGCCAGCAGCTGAT
Delta G	-3.07 kcal/mole
Base Pairs	
buse runs	.
5' TAGTCG	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
3'	CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT
,	GMI I TACAMENTO CONCENT TO CONCENT OF THE CONCENT O
	-3.07 kcal/mole
Base Pairs	2
-	
5' TAGTCG	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
	: :::: :
3'	CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT

5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: :: : : : : :		
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		•
Delta G -3.07 kcal/mole		
Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: : : : : : : : : : : : : : : : : :		
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G -1.95 kcal/mole Base Pairs 2		·
Dase Falls 2		•
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: ::		
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	•	
•		
	-	,
Delta G -1.94 kcal/mole		
Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
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3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	•	
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Delta G -1.94 kcal/mole Base Pairs 2		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	•	
: :: : :		
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G -1.94 kcal/mole		
Base Pairs 2	•	
•		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: :: : :	CAM	
3 ' CGATTAACAAAAACCTACGACATTGCCAGCAGCTG	SAT	

Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: 3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.94 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : :: : :	
: :: : : 3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.94 kcal/mole	
Base Pairs 2	•
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: :	
3 CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.94 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTGGGCC ::	
3 · CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: :	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT .	
Delta G -1.6 kcal/mole	
Base Pairs 2	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: ::::	
3 CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
·	

Delta G

-1.94 kcal/mole

Delta G -1.6 kcal/mole Base Pairs 2	
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: CGATTAACAAAAACCTACGACATTGCCA	AGCAGCTGAT
	•
Delta G -1.57 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC::	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.57 kcal/mole Base Pairs 2	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: : :: : : 3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.57 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: : : : :	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.34 kcal/mole Base Pairs 2	
5 ' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : ::	
: : : :: 3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.34 kcal/mole	
Base Pairs 2	
TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : :: ::	

3' CGATTAACAAAACCTACGACATTGCCAGCAGCTGAT

Delta G -1.34 kcal/mole	
Base Pairs 2	
•	
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -1.34 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
•	
Delta G -1.34 kcal/mole	
Base Pairs 2	
5 ' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -0.96 kcal/mole	
Base Pairs 2	
·	•
5 ' TAGTCGACGACCGTTAGGGTTTACCTTC'	PTTGGGCC
3' CGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
- 11 - 12 - 12 - 12 - 12 - 12 - 12 - 12	
Base Pairs 2	
F I TO OTHER DESCRIPTION OF COMPANY CO	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : : :	
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For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

Innovation & Precision In Nucleic Acid Synthesis

↓↓ OligoAnalyzer 3.0	•	
# Bases		
AG TCG ACG ACC GTT AGG GTT TAC CTT CTT TGG GCC	1 ·	ANALYZE
_	Target Type DNA	HAIRPIN
•	Oligo Conc 0.25 µM	SELF-DIMER
	Na ⁺ Conc 50 mM	HETERO-DIMER
	J _{-3'}	NCBI BLAST
	·	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	(LNA CONVERSION
مناوي المنفضي والمستدعين المرازي المراقع المرازي المستدعا	and the same of th	
SULTS BASE NOTATION 5' MODS IN	TERNAL MODS 3' MODS	and the state of t
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mary Sequence		
TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC -3'		
ondary Sequence	•	
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG -3'		
10,00ATAGCTAGTCGTTGGGCTTTGTTGCCTTGGTG		
kimum Delta G -72.71 kcal/mole	·	
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kimum Delta G -72.71 kcal/mole		· · · · · · · · · · · · · · · · · · ·
ta G -7.87 kcal/mole	·	· · · · · · · · · · · · · · · · · · ·
kimum Delta G -72.71 kcal/mole	·	
ta G -7.87 kcal/mole se Pairs 5		
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT	TGGGCC	
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT :	TGGGCC	
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT	TGGCC	
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT :	TGGCC	
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT :	TGGCC	
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	TGGCC	
ta G -7.87 kcal/mole ta G -7.87 kcal/mole se Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT ta G -6.68 kcal/mole	TGGCC	
ta G -7.87 kcal/mole ta G -7.87 kcal/mole ta G -7.87 kcal/mole TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	TGGCC	
ta G -7.87 kcal/mole se Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT ta G -6.68 kcal/mole se Pairs 3		
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT ta G -6.68 kcal/mole se Pairs 3 TAGTCGACGACCGTTAGGGTTT		
ta G -7.87 kcal/mole ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT ta G -6.68 kcal/mole te Pairs 3 TAGTCGACGACGACCGTTAGGGTTT : : :		
ta G -7.87 kcal/mole te Pairs 5 TAGTCGACGACCGTTAGGGTTTACCTTCTT : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT ta G -6.68 kcal/mole se Pairs 3 TAGTCGACGACCGTTAGGGTTT		

: : : : : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta Ġ -6.21 kcal/mole Base Pairs 3
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -6.21 kcal/mole Base Pairs 3
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: 3 · GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.19 kcal/mole Base Pairs 3
TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.19 kcal/mole Base Pairs 3
TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.12 kcal/mole Base Pairs 4
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

Delta G -5.02 kcal/mole

5' TAGTCO	GACGACCGTTAGGGTTTACCTTCTTTGGGCC		
	III · · ·		
3 '	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGG	CT	
			
		·	
Delta G	-4.67 kcal/mole .		
Base Pairs	3	•	
5' TAGTCO	GACGACCGTTAGGGTTTACCTTCTTTGGGCC		
	::		
3 '	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
,	•		
	•		
Delta G	-3.61 kcal/mole		
Base Pairs	•		
5'	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
3' GAGGA	CCGAAGTTTCGGGTTGCTGATCGATAGGCT		
		·	
		1000	
		•	
	-3.54 kcal/mole		
Base Pairs	; 3	•	
5' TAGTC	GACGACCGTTAGGGTTTACCTTCTTTGGGCC		
3'	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
Delta G	-3.14 kcal/mole		
Base Pairs	3 2		
5 '	GACGACCGTTAGGGTTTACCTTCTTTGGGCC		
J INGIC	: : : : :		
3 '	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
,	GAGGACCGAAGIIICGGGIIGCIGAICGAIAGGCI		
Dolta G	-3.07 kcal/mole		
Base Pairs			
ause rails			
5'	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
	: : : : : : : : : : : : : : : : : : : :		
3' GAGGA	CCGAAGTTTCGGGTTGCTGATCGATAGGCT		

Delta G -3.07 kcal/mole
Base Pairs 2

: : : : : 3
Delta G -3.07 kcal/mole Base Pairs 2
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :::: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -3.07 kcal/mole Base Pairs 2
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -3.07 kcal/mole Base Pairs 2
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -3.07 kcal/mole Base Pairs 2
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : :: : : : : : : : : : : : : : : : :
Delta G -3.07 kcal/mole Base Pairs 2
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : :: : : : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

	•		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC			
:: ::			
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT			
Delta G -3.07 kcal/mole		•	
Base Pairs 2			
Dase rails 2			
·5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC			
		•	•
0.003.0003.30003	TTCGGGTTGCTGATCGATAGGCT		•
3 GAGGACCGAAGTT	Preded The Idaleda Ladde I		
		•	
Delta G -2.56 kcal/mole			
Base Pairs 3			
	·		•
5 TAGTCGACGACCGTTAGGGT	TTACCTTCTTTGGGCC		
111			
• • •	•		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT			
		•	
Delta G -2.56 kcal/mole			
Base Pairs 3			
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGG	cc		
: ::: :		•	
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT			
5 GAGGACCGAAGIIICGGGIIGCIGAICGAIAGGCI			
· .			
		•	
Delta G -1.94 kcal/mole			
Base Pairs 2			
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	·		•
: ::			
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT			
			•
Delta G -1.6 kcal/mole		•	
Base Pairs 2		•	
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC			
:::::::::::::::::::::::::::::::::::::::		•	
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT			

Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:::: :: :::		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
		**
Delta G -1.6 kcal/mole		
Base Pairs 2		
5 ' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : :		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	•	
J GAGGREGIZIOTEGIZIONE		

Delta G -1.6 kcal/mole		
Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		,
: : : : : : :		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
Delta G -1.6 kcal/mole		
Base Pairs 2		
•		•
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
: : : :		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
Delta G -1.6 kcal/mole		
Base Pairs 2		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: : : : :		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
J GROCKEG/WG111cccc11Gc1GMCCC1		
Delta G -1.6 kcal/mole		
Base Pairs 2		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
:: :		
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		

Delta G

-1.6 kcal/mole

Base Pairs 2	
5'	· TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
	11
3' GAGGACCG	AAGTTTCGGGTTGCTGATCGATAGGCT
5 ONGONECO	
Delta G -1	57 kcal/mole
Base Pairs 2	
base rails 2	
5' TAGT	CGACGACCGTTAGGGTTTACCTTCTTTGGGCC
: :	:: :: : :
3' GAGGACCG	AAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1	57 kcal/mole
Base Pairs 2	
5' TAGTCGAC	CACCGTTAGGGTTTACCTTCTTTGGGCC
	: : :
3 '	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -0	0.96 kcal/mole
Base Pairs 2	
	\cdot
_	
5 '	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
	:.
3' GAGGACCO	CAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G - (0.96 kcal/mole
Base Pairs 2	
· .	
5' 7	PAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC
_	: : : :
3' GAGGACCO	SAAGTTTCGGGTTGCTGATCGATAGGCT

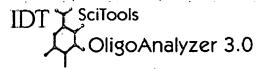
For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

-1.57 kcal/mole

Delta G

Innovation & Precision In Nucleic Acid Synthesis

Instructions | Definitions | Feedback



Bases

5'-TAG TCG ACG ACC GTT AGG GTT TAC CTT CTT TGG GCC

Target Type DNA
Oligo Conc 0.25 µM

HATRPIN

SELF-DIMER

Na+ Conc 50 mM

NCBI BLAST

TM MISMATCH

CLEAR SEQUENCE ADD TO ORDER

DEFAULT SETTINGS

LNA CONVERSION

RESULTS

BASE NOTATION

5' MODS

INTERNAL MODS

3' MODS

Primary Sequence

5'- TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC -3'

Secondary Sequence

5'- TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA -3'

Maximum Delta G -72.71 kcal/mole

Delta G -7.87 kcal/mole

Base Pairs 5

TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

: ||||

3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -6.9 kcal/mole

Base Pairs 4

5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -6.68 kcal/mole ·

Delta G -4.41 kcal/mole

5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
: : : :		
J AICCCAROOMATITION AND TOUR OF THE COMMISSION O		
Delta G -3.61 kcal/mole		
Base Pairs 2	·	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
: : : : : : :	•	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	•	
	·	
Delta G -3.61 kcal/mole		
Base Pairs 2	·	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
: :: : :		
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
Delta G -3.61 kcal/mole		
Base Pairs 2		
		•
EL TRACTICA CON COOPERA COOPER		
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	•	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	•	
		· · · · · · · · · · · · · · · · · · ·
Delta G -3.52 kcal/mole		
Base Pairs 3		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
: : 3	•	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
•	·	
Delta G -3.52 kcal/mole		
Base Pairs 3		
•		
5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC		
· · · · · · · · · · · · · · · · · · ·		
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGC	т	

Delta G -3.29 kcal/mole Base Pairs 3

5' TAGTCGACGACCGTTAGGGT				•	
:::		CC 3 M3 CC CM			
3' ATCGCA	AGGATATTTTGGTAAGTGCTGAT	CGATAGGCT			
Delta G -3.14 kcal/mole					
Base Pairs 2					
5' TAGTCGACGACCGTTAGGGT	[℩] ͲͲ∆ ℂℂͲՊℂͲ <mark>Ͳ</mark> Ͳር <mark>ር</mark> ርԸԸ				
J INGICONCONCOLLINGOL	11				•
3'	ATCGCAAGGATA	TTTTGGTAAGTGCTG!	ATCGATAGGCT		
		· · · · · · · · · · · · · · · · · · ·			
Delta G -3.07 kcal/mole	•				
Base Pairs 2					
5' TAGTCGACO	ACCGTTAGGGTTTACCTTCTTTG	GGCC			
::	: : :				
3' ATCGCAAGGATATTTTGGTA	LAGTGCTGATCGATAGGCT				
			· · · · · · · · · · · · · · · · · · ·		
D-M- C 2.07 (con)/mole					
Delta G -3.07 kcal/mole Base Pairs 2					
base runs 2	·				
				•	•
5' TAGTCGACGACCGTTAGGGT					
::: : : : : : : : : : : : : : : : : :	, ,			•	
3 ATCGCAAGGATATTTTGGTA	MGIGCIGAICGAIAGGCI				
	· · · · · · · · · · · · · · · · · · ·				
,					
Delta G -3.07 kcal/mole					
Base Pairs 2					
				•	
5 TAGTCGACGACCGTTAGGGT	PTTACCTTCTTTGGGCC				
	: 11				
3' A	rcgcaaggatattttggtaagtgc	TGATCGATAGGCT		,	
		·			
	· · · · · · · · · · · · · · · · · · ·				
			٠		
Delta G -3.07 kcal/mole					
Base Pairs 2					
5 TAGTCGACGACCGTTAGGG					
	: ::				
3' ATCGCAAGGATATTTTY	GGTAAGTGCTGATCGATAGGCT				

			•
5 TAGTCGACGACCGTTAGGGTTTACCT	ጥርምምምርርርርር		
3 TAGICGACGACCGITAGGGITTACC	1.1		
	, : -		
•	ATCGCAAGGATATTTTGGTAAGTGCTGATC	GATAGGCT	
Delta G -2.56 kcal/mole			
Base Pairs 3	· ·		
		•	
5 '	TAGTCGACGACCGTTAGGGTTTACCTTCTT	rTGGGCC	
	:		
3' ATCGCAAGGATATTTTGGTAAGTGC	GATCGATAGGCT		
•	,		
	,		
Delta G -2.56 kcal/mole			
Base Pairs 3			
5436 (4113 3			
	TTAGGGTTTACCTTCTTTGGGCC		
: : ::	:		
3 ' ATCGCAAGGATATTTTGGTAAGTGC	САТССАТАСССТ		
A I COCANOGATATITIOG TAAGTOC	GATCOATAGGET		
•			
	•		
Delta G -1.94 kcal/mole			
Base Pairs 2			
5 ' TAGTCGACGACCGTTAGGGTTTACC'	TCTTTGGGCC		
	: :		
. : : :			
3' ATCGCAAGGATATTTT	GTAAGTGCTGATCGATAGGCT	,	
			4 2. Lin
Delta G -1.94 kcal/mole	·		
Base Pairs 2	•		
Dase Falls 2			
5 ' TAGTCGACGACCGTTAGGGTTTACC'	TCTTTGGGCC	•	
: ::	: []		
	GGTAAGTGCTGATCGATAGGCT		
AICGCAAGGAIAIII	GGTAAGTGCTGATCGATAGGCT		
Delta G -1.94 kcal/mole			
Base Pairs 2			
•			
E L			
5 TAGTCGACGACCGTTAGGGTTTACC			•
: :	:	•	
	PATTTTGGTAAGTGCTGATCGATAGGCT		
J ATCOCAROGA			

Delta G -1.9 Base Pairs 2	4 kcal/mole
base rails 2	
5 TAGTCGACGA	ACCGTTAGGGTTTACCTTCTTTGGGCC
2.1	A MOCCOA A COA MA MUMBUCCERA A CIRCOMO A MOCCA PIA CGCP
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.9	4 kcal/mole
Base Pairs 2	,
5' TAGTCGACGA	ACCGTTAGGGTTTACCTTCTTTGGGCC
3'	: ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
3 '	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.6	kcal/mole
Base Pairs 2	
÷	ACGACCGTTAGGGTTTACCTTCTTTGGGCC
	: : :: : : ATATTTTGGTAAGTGCTGATCGATAGGCT
3 ATCGCAAGGA	TATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.6	kcal/mole
Base Pairs 2	
5' TAGTCGA	CACCGTTAGGGTTTACCTTCTTTGGGCC
	,GACCGTTAGGGTTTACCTTCTTTGGGCC
:: 31 ATCCCAACC	TATTTTGGTAAGTGCTGATCGATAGGCT
J ATCGCAAGG	THITITION TO TO TO TO THOUSE I
·	
Delta G -1.6	kcal/mole
Base Pairs 2	
F. maggarage	
5 TAGTCGACG	ACCGTTAGGGTTTACCTTCTTTGGGCC
3 '	: : : : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
3	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.5	7 kcal/mole
Base Pairs 2	· · · · · · · · · · · · · · · · · · ·
.	,
5 '	TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC .
31 AMOGOS 3 C = 1	
5 ATCGCAAGG	ATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -1.57 kcal/mole	
Base Pairs 2	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: :::::	
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
•	
Delta G -1.57 kcal/mole	
Base Pairs 2	
5 · TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
: [] : ::	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -1.34 kcal/mole	
Base Pairs 2	
	•
5' TAGTCGACGGTTAGGGTTTACCTTCTTTGGGCC	
:: :	•
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -0.96 kcal/mole	
Base Pairs 2	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : :	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : :	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : :	
Base Pairs 2 5	
Base Pairs 2 5	
Base Pairs 2 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : 3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2	
Base Pairs 2 5	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2 5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: ::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole	
5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2 5 TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC : : : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: ::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole	
Base Pairs 2 5	
Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC ::: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Base Pairs 2 5' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC :: ::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -0.96 kcal/mole	

Delta G 🕟	-0.96 kcal/mole
Base Pairs	2

5 ' TAGTCGACGACCGTTAGGGTTTACCTTCTTTGGGCC

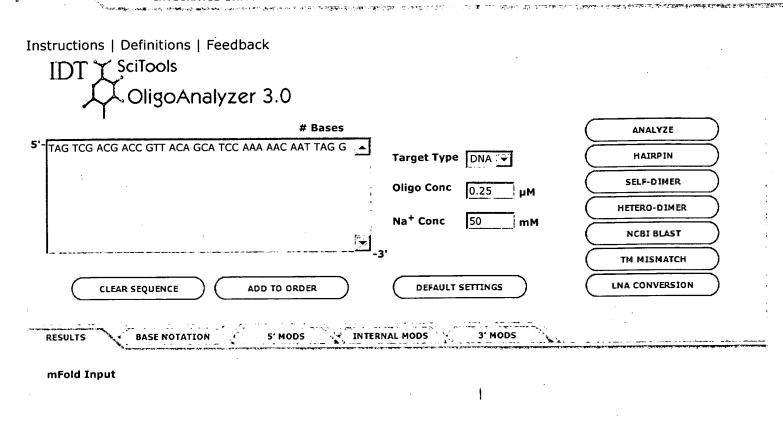
|| : : :

 ${\tt ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT}$

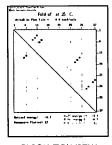
For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

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General Information



Batch Date: Sequence:

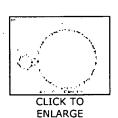
Sequence Name: 37 Base Oligo 11/8/2006

TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG

ADD TO ORDER

CLICK TO VIEW DOT PLOT

Structure 1



-0.72 kcal.mole⁻¹ ΔG

T_M 34.4 °C

-23 kcal.mole⁻¹ ΔH

-74.8 cal.K⁻¹mole⁻¹ ΔS

CONNECTIVITY

DETAILS

3 ' .

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Instructions Definitions Feedback		
IDT Y SciTools		and the second s
OligoAnalyzer 3.0	•	
# Bases		ANALYZE
5'-TAG TCG ACG ACC GTT ACA GCA TCC AAA AAC AAT TAG G	Target Type DNA	HAIRPIN
		SELF-DIMER
		HETERO-DIMER
	Na ⁺ Conc 50 mM	NCBI BLAST
	3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTER	RNAL MODS 3' MODS	e e e e e e e e e e e e e e e e e e e
HOMO-DIMER ANALYSIS		
Dimer Sequence 5'- TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG -3'		
Maximum Delta G -69.59 kcal/mole		
Delta G -9.45 kcal/mole Base Pairs 6		
	AGCATCCAAAAACAATTAGG	
: : 3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G -6.53 kcal/mole Base Pairs 4		
TAGTCGACGACCGTTACAGCA	ATCCAAAAACAATTAGG	
3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta C 5 26 kgal/mala		
Delta G -5.36 kcal/mole Base Pairs 4		
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		

GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT

Base Pairs 3	
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	•
3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -3.61 kcal/mole Base Pairs 2	
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: : : :: 3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -3.61 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: 3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -3.61 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : 3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT	
Delta G -3.29 kcal/mole Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :::::::::::::::::::::::::::::::	
Delta G -3.14 kcal/mole Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : : 3' GGATTAACAAAAACCTTACGACAGCAGCTGAT	·

Delta G

-4.95 kcal/mole

Delta G -3.07 kcal/mole Base Pairs 2		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
3' GGATTAACAAAACCTACGACATTGCCAGCAGCTGAT		
		•
Delta G -3.07 kcal/mole Base Pairs 2		
base Pairs 2		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
:: ::::		
3 GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G -1.94 kcal/mole		
Base Pairs 2		
·		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
		<u></u>
Delta G -1.94 kcal/mole		
Base Pairs 2		
E L MACHIGO A COA COCCIUMA CA COA MOCA A A A A CA A MINA CO		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: : : : :		
3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
	•	
Delta G -1.94 kcal/mole		•
Base Pairs 2		
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
: : :: ::		
3' GGATTAACAAAACCTACGACATTGCCAGCAGCTGAT		
Delta G -1.94 kcal/mole		
Base Pairs 2		
	•	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG 		
3' GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		

•

Delta G Base Pairs	-1.94 kcal/mole			
		•		
5' TAGTCO	ACGACCGTTACAGCATCCAAAAACAATTAGG			
	: :: :			
3'	GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT			
			<u> </u>	
- " -	4.04 bank/arak			
Base Pairs	-1.94 kcal/mole 2			
5' TAGTCO	ACGACCGTTACAGCATCCAAAAACAATTAGG			
2.	: :: :			
3 '	GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT			
Delta G	-1.94 kcal/mole			
Base Pairs		•		
5' TAGTCO	BACGACCGTTACAGCATCCAAAAACAATTAGG			
3 '	:: GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT			
3	GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT			
	· · · · · · · · · · · · · · · · · · ·			
Delta G	-1.57 kcal/mole			
Base Pairs				
5'.	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG			
21 00 000	: : : : : : : : : : : : : : : : : :			
3 GGATTA	ACAAAAACCTACGACATTGCCAGCAGCTGAT			
Delta G	-1.57 kcal/mole		•	
Base Pairs				
	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG			
	: : : : :: : : :			
3 GGATTA	ACAAAAACCTACGACATTGCCAGCAGCTGAT			
				····
Delta G	-1.47 kcal/mole			
Base Pairs	·			
5' TAGTCO	SACGACCGTTACAGCATCCAAAAACAATTAGG			
3 '	: :: : GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT			
3	GGAT TAMCAMAMACC TACGACAT TGCCAGCAGC TGAT			

Delta G -1.34 kcal/mole

	CAGCATCCAAAAACAATTAGG	
• • • • • • • • • • • • • • • • • • • •	: :	·
GGATTAACAAAAACCTACGACATTGCCAGCA	AGCTGAT	•
· ,		•
		·
Delta G -1.34 kcal/mole		
Base Pairs 2		
	•	
TAGTCGACGACCG	FTTACAGCATCCAAAAACAATTAGG	
::	::	
3 ' GGATTAACAAAAACCTACGACATTGCCAGCA	AGCTGAT	
		·
- II 0 124 beel/made	•	
Delta G -1.34 kcal/mole		
Base Pairs 2		
•	·	
5 · TAGTCGACGACCGTTACAGCATC	CCAAAACAATTAGG	
: : : : : :		
	•	•
3. GGATTAACAAAAACCTACGACATTGCCAGCA	AGC I GAI	
•		
	•	
Delta G -1.34 kcal/mole		
Base Pairs 2		
		•
	A A A A O A A MUDA C C	
5 ' TAGTCGACGACCGTTACAGCATCCAA		
	•	
3 ' GGATTAACAAAAACCTACGACATTGCCAGCA	AGCTGAT	•
		•
Delta G -0.96 kcal/mole		
Base Pairs 2		
	•	
5'	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
		• • • • • • • • • • • • • • • • • • • •
3' GGATTAACAAAAACCTACGACATTGCCAGCA	• •	
		•
Delta G -0.96 kcal/mole	•	
Base Pairs 2		
E I	C	
5 TAGTCGACGACCGTTACAGCATCG		
: : :		•
3 GGATTAACAAAAACCTACGACATTGCCAGC	AGCTGAT	
	•	

Delta G -0.96 kcal/mole Base Pairs 2

: : : : : : : : : : : : : : : : : :		and the state of t	
Delta G -0.96 kcal/mole Base Pairs 2			
5' TAGTCGACGACCGTTACAGCATCC : 3' GGATTAACAAAA	AAAAACAATTAGG : :: ACCTACGACATTGCCAGCAGCTGAT		
Delta G -0.96 kcal/mole Base Pairs 2	· · · · · · · · · · · · · · · · · · ·		
5' TAGTCGACGACCGTTACAGCATCC.	AAAAACAATTAGG GGATTAACAAAAACCTACGACATTGCCAGCAGCTGAT		
,	llysis contact our Technical Support Group		

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Innovation & Precision
In Nucleic Acid Synthesis

The state of the s	प्रकार पुत्र राज्याना क्रिक्ट कर है। इस क्रिक्ट के क्रिक्ट क्रिक्ट क्रिक्ट क्रिक्ट क्रिक्ट क्रिक्ट क्रिक्ट क्र इस क्रिक्ट पुत्र राज्याना क्रिक्ट क्रि	A STATE OF THE PARTY OF THE PAR
Instructions Definitions Feedback		
IDT Y SciTools		
OligoAnalyzer 3.0		
# Bases		ANALYZE
5'-TAG TCG ACC GTT ACA GCA TCC AAA AAC AAT TAG G	Target Type DNA 🔻	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
		HETERO-DIMER
↓i	Na ⁺ Conc 50 mM	NCBI BLAST
	3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
	and the second s	
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	
Primary Sequence		
5'- TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG -3'		
Secondary Sequence 5'- TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG -3'		
Maximum Delta G -70.77 kcal/mole	. •	•
Delta G -7.87 kcal/mole	·	
Base Pairs 5		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAA	TTAGG	
: :	·	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
Delta G -6.97 kcal/mole		
Base Pairs 4		
		•
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :: :: :		•
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		

Delta G -6.68 kcal/mole

: : : 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -6.53 kcal/mole Base Pairs 4
5 ' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : 3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -6.12 kcal/mole Base Pairs 4
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.84 kcal/mole Base Pairs 4
5 ' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : 3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.19 kcal/mole Base Pairs 3
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.19 kcal/mole Base Pairs 3
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

Delta G -4.74 kcal/mole

5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	·	
		•
		<u></u>
		•
Delta G -4.74 kcal/mole		
Base Pairs 3		
base Pairs 3		
·	•	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	•	
D. D. A. C. A. Karal Association		
Delta G -4.64 kcal/mole		•
Base Pairs 3		
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		•
:		
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
3 GAGGACCGAAGIIICGGGIIGCIGAICGAIAGGCI		
	-	
•		÷
Delta G -3.9 kcal/mole		
Base Pairs 3		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
: :: :: : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
5 GAGGACCGAAGIIICGGGIIGCIGAICGAIAGGCI		
•	•	
	•	•
Delta G -3.9 kcal/mole		•
Base Pairs 3		
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT		
	,	
		•
Delta G -3.89 kcal/mole		
Base Pairs 3		
E.L. MA OMOGA GOA GOOMMA GA GOA MGGA A A A A A A A A A A A A A A A A A		
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		•
: :		
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	•	
	•	•
		

Delta G -3.89 kcal/mole Base Pairs 3

5 TAGTCGACGACCGTTACAGCATCCAAAAACCAATTAGG	
: : : GAGGACCGAAGTTTCGGGTTGCTGATCGA	TA CCCM
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGA'	TAGGCT
Delta G -3.29 kcal/mole	
Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -3.07 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
:: : : :	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
	•
Delta G3.07 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
	•
Delta G -3.07 kcal/mole	
Base Pairs 2	
F. T. CTGG, GG, GGGTT, G, GG, TGG, L, L, L, C, L, TTT, GG	•
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : ::	
GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
J	
Delta G -3.07 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
·	
3 ' GAGGACCGAAGTTT	CGGGTTGCTGATCGATAGGCT

5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :: : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -2.56 kcal/mole Base Pairs 3
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.95 kcal/mole Base Pairs 2
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.95 kcal/mole Base Pairs 2
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: : : : :: : 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.94 kcal/mole Base Pairs 2
5 · TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG 3 · GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.94 kcal/mole Base Pairs 2
5 ' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : 3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

base Pairs 2
5 · TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
:
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.94 kcal/mole
Base Pairs 2
\cdot
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
3 · GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.6 kcal/mole
Base Pairs 2
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.6 kcal/mole
Base Pairs 2
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
: Π
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
5 · TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
3 · GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
J GASGACCGAAGIIICGGIIGGCI
Delta G -1.34 kcal/mole
Base Pairs 2
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
: : : :
3 · GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

Delta G

-1.94 kcal/mole

Base Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :	relta G -1.34 kcal/mole	
: : :: :: : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT elta G -1.34 kcal/mole ase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: :: :: : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT elta G -0.96 kcal/mole ase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: : : :: :	ase Pairs 2 ,	
: : :: :: GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT elta G -1.34 kcal/mole ase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT elta G -0.96 kcal/mole ase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :		₽ .
elta G -1.34 kcal/mole ase Pairs 2 TAGTCGACGACGTTACAGCATCCAAAAACAATTAGG ::::::::::::::::::::::::::::::::	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
elta G -1.34 kcal/mole ase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG ::::::::::::::::::::::::::::::::	: : : : : : : : : : : : : : : : : : : :	•
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :::::::::::::::::::::::::::::::	' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG ::::::::::::::::::::::::::::::::		
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :::::::::::::::::::::::::::::::		
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG ::::::::::::::::::::::::::::::::		
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : : GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT Pelta G -0.96 kcal/mole Gase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :	relta G -1.34 kcal/mole	
::::::::::::::::::::::::::::::::::::::	ase Pairs 2	
::::::::::::::::::::::::::::::::::::::	· ·	
::::::::::::::::::::::::::::::::::::::	TACTOCACCACCCTTACAGCATCCAAAAACAATTAGG	•
GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT Delta G -0.96 kcal/mole Dase Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :		·
Delta G -0.96 kcal/mole Base Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :	11	
Base Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :	GAGGACCGAAGTTTCGGGTTGCTGATTCGGTT	
Base Pairs 2 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :		
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :		
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :	nelta G =0.96 kcal/mole	•
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : :		
: 11 - :		
: II · · ·		
: : ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	: :	
	GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	•
		•
	or questions regarding the Dimer Analysis contact our Technical Support Gro 800-328-2661 or e-mail TechSupport@idtdna.com	pup

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nstructions Definitions Feedback		
istractions boilinitions recently		en e
IDT L'Scilools		•
Oligo Analyzer 3 0	•	
↓ OligoAnalyzer 3.0		
# Bases		
		ANALYZE
TAG TCG ACG ACC GTT ACA GCA TCC AAA AAC AAT TAG G	Target Type DNA →	HAIRPIN
	Target Type DNA	
!	Oligo Conc 0.25	(SELF-DIMER)
	Oligo Conc 0.25 µM	
	Na ⁺ Conc 50 mM	HETERO-DIMER
	Ma Conc 150 MM	NCBI BLAST
	3'	
-		(TM MISMATCH)
(CLEAR SEQUENCE) (ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
	•	
RESULTS BASE NOTATION 5' MODS INTER	RNAL MODS 3' MODS	
The second secon	To the control of the second s	the state of the s
rimary Sequence		
5'- TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG -3'	•	
Secondary Sequence		
5'- TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA -3'		
1000		
Maximum Delta G -70.41 kcal/mole		
TO A TO THE TOTAL OF THE TOTAL		
Delta G -7.87 kcal/mole		
Base Pairs 5		
	ACAATTAGG	
TAGTCGACGACCGTTACAGCATCCAAAAA	ACAATTAGG	
: :		
: :	ACAATTAGG	
: :		
: :		
: : 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Pelta G -7.18 kcal/mole		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Pelta G -7.18 kcal/mole Base Pairs 5		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole		
: : B ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5		
: : B ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 C TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
: : B ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :::		
: : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :::		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :::		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Peltà G -7.18 kcal/mole Base Pairs 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :::		
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : ::: ATCGCAAGGATATTTTGGTAAGTGCTGATCGA		
: : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT Delta G -7.18 kcal/mole Base Pairs 5 5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : :::		

3'	: : : :: ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -6 Base Pairs 3	•
5' 3' ATCGCAAC	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : GGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -6 Base Pairs 4	
5' 3' ATCGCAAC	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : GGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G - 6 Base Pairs 4	
	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG : : : : : GGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G - Base Pairs 4	5.83 kcal/mole
5' TAGTCGAC	CGACCGTTACAGCATCCAAAAACAATTAGG : : :: : : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G - Base Pairs 3	5.19 kcal/mole
5' 3' ATCGCAA	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG :: GGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -5.19 kcal/mole

5 TAGTCGACGACCGTTACAGCATCCAAAAACA	ATTAGG
: []	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
3 AICGCAAGGATAIIIIGGTAAGIGCIGAICGATAGGCI	
Delta G -5.02 kcal/mole	
Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: : ::::	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
	•
- 10 - 10 - 10 - 10 - 10 - 10 - 10 - 10	
Delta G -4.74 kcal/mole	
Base Pairs 3	
5 ' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
:: : : : :	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
	•
Delta G -4.74 kcal/mole	
Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: : : :: :	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
••••••••••	
·	
Delta G -4.64 kcal/mole	
Base Pairs 3	
EL MACMOCA COA COCUMA CACCAMOCA A A A A CA AMMACO	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: :: :	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -4.41 kcal/mole	
Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: : : :: : : : : :	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	

Delta G -3.89 kcal/mole Base Pairs 3

TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
.: :	•
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -3.89 kcal/mole	•
Base Pairs 3	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -3.61 kcal/mole	
Base Pairs 2	
Dase Falls 2	
	·
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: :: :	·
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
•	•
Delta G -3.61 kcal/mole	
Base Pairs 2	
	·
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
	•
	•
Delta G -3.43 kcal/mole	•
Base Pairs 3	
TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: : : : :: : : : : : : : : : : :	
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
J Aledemodalalliddimaldeldaledaladdel	
Delta G -3.07 kcal/mole	
Base Pairs 2	
DUSC I UIIS 2	·
•	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
	·

Delta G -1.95 kcal/mole

Delta G -1.94 kcal/mole Base Pairs 2	
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: :: :	
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
•	
Delta G -1.94 kcal/mole	
Base Pairs 2	•
5 TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	·
:	
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -1.94 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: 	
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
	·
Delta G -1.94 kcal/mole	•
Base Pairs 2	
	·
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	·
:	
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	•
•	
Delta G -1.57 kcal/mole	
Base Pairs 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGC	3
Π .	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delha C. 1 57 keel/mele	
Delta G -1.57 kcal/mole Base Pairs 2	
2000 1 2000 - 2	
5' TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG	
: : :: :	
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	

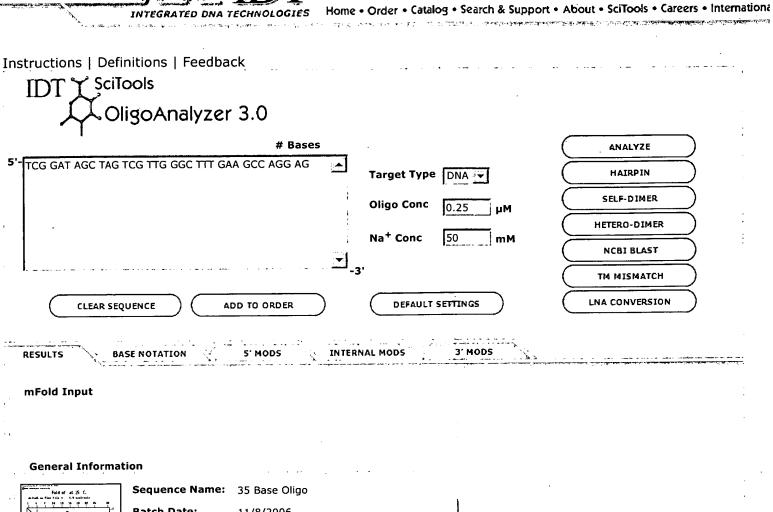
Base Pairs	2
	·
הי יים דאמיי	CGACGACCGTTACAGCATCCAAAAACAATTAGG
3 ATCGCAA	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
	-1.47 kcal/mole
Base Pairs	2
-	·
5	ACGACCGTTACAGCATCCAAAAACAATTAGG
J INGICO	: : :
3 '	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
3	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
	-1.34 kcal/mole
Base Pairs	2
5'	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
3' ATCGCAZ	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
3 11100011	
Delta G	-1.34 kcal/mole
Base Pairs	
buse i ans	
5 '	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
	: : :: ::
3' ATCGCA	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-1.34 kcal/mole
Base Pairs	2
5'	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
3' ATCGCA	AGGATATTTTGGTAAGTGCTGATAGGCT
	·
	-1.34 kcal/mole
Base Pairs	2
5'	TAGTCGACGACCGTTACAGCATCCAAAAACAATTAGG
-	:: : :

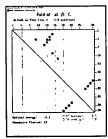
-1.57 kcal/mole

 ${\tt 3} \verb|' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT|\\$

Delta G -0.96 kcal/mol	le	•	•
Base Pairs 2			
	22 CO 2 DCC 2 2 2 2 2 C 2 2 DDC 2 C C		
5 TAGTCGACGACCGTTAC	CAGCATCCAAAAACAATTAGG	•	
	:		
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
	•	·	
			
•			
Delta G -0.96 kcal/mo	le		
Base Pairs 2		·	
5 ·	CAGCATCCAAAAACAATTAGG	·	
· . II	: : : : : : :		
3 ATCGCAAGGATA	ATTTTGGTAAGTGCTGATCGATAGGCT		
3 ATCGCAAGGATA	ATTTTGGTAAGTGCTGATCGATAGGCT	•	
	•		
Delta G -0.96 kcal/mo	ie .	•	
Base Pairs 2			
·			
5' TAGTCGACGACCGTTAG	CAGCATCCAAAAACAATTAGG		
•	: 11		
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGG	GCT .	
For questions recording the	Dimer Analysis contact our Technical Support Group		
1-800-328-2661 or e-mail	FechSupport@idtdna.com	•	

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Batch Date: 11/8/2006

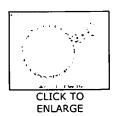
Sequence:

TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG

ADD TO ORDER

CLICK TO VIEW DOT PLOT

Structure 1



-4.13 kcal.mole⁻¹ ΔG

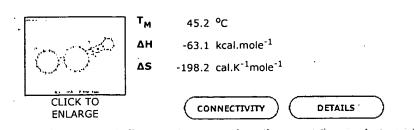
TM 58.7 °C

-40.4 kcal.mole⁻¹ ΔΗ

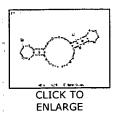
-121.8 cal.K⁻¹mole⁻¹ ΔS

CONNECTIVITY **DETAILS**

Structure 2







ΔG -2.91 kcal.mole⁻¹

T_M 40.6 °C

ΔH -58.2 kcal.mole⁻¹

ΔS -185.5 cal.K⁻¹mole⁻¹

CONNECTIVITY)

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DETAILS



Instructions Definitions Feedback
IDT Carlook OligoAnalyzer 3.0
Bases 5'-TCG GAT AGC TAG TCG TTG GGC TTT GAA GCC AGG AG Target Type DNA Oligo Conc 0.25 µM HETERO-DIMER Na+ Conc 50 mM
CLEAR SEQUENCE ADD TO ORDER DEFAULT SETTINGS NCBI BLAST TM MISMATCH LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTERNAL MODS 3' MODS
HOMO-DIMER ANALYSIS
Dimer Sequence 5'- TCGGATAGCTAGTCGTTGGAGCCAGGAG -3'
Maximum Delta G -70.77 kcal/mole
Delta G -9.75 kcal/mole Base Pairs 5
5 TCGGATAGCTAGTCGTTGGAGCCAGGAG : ::::: : 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -8.26 kcal/mole Base Pairs 6
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG :: :: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -5.02 kcal/mole Base Pairs 3
5 ' TCGGATAGCTAGTCGTTGGGCCTTTGAAGCCAGGAG : :::: 3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

Delta G -4.74 kcal/mole	
Base Pairs 3	
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
· : :: :: :: :: : : : : : : : : : :	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -4.74 kcal/mole	
Base Pairs 3	
	•
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG	
: :	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -4.16 kcal/mole	•
Base Pairs 4	
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
: : : :	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
5 GAGGACCGAAGIIICGGIIIGGGI	
	•
Delta G -3.61 kcal/mole	
Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
5 Grooneconnormes and a second	
Delta G -3.14 kcal/mole	
Base Pairs 2	
	•
S. L. MOGOLINI GOTTA OTTO OTTO OTTO OTTO OTTO OTTO OTT	
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG	
:: : : : : : : : : : : : : : : : : :	
5 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
	•
Delta G 3 14 kcal/mole	
Delta G -3.14 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG	
: :	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	

Base Pairs 2
5. TCGGATAGCTAGTCGTTGGAGCCAGGAG
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -3.07 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
· ::
GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.95 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
Delta G -1.94 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
•
Delta G -1.94 kcal/mole
Base Pairs 2
\cdot
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT
•
Delta G -1.6 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGGGCTTTGAAGCCAGGAG
::
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT

Delta G

-3.07 kcal/mole

Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGGGCTTTGAAGCCAGGAG	
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.6 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG	
er en	
GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole Base Pairs 2	
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole Base Pairs 2	
5 TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
:: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole	
Base Pairs 2	
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG	
∏ : : ::	
3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	

Delta G -1.57 kcal/mole Base Pairs 2

: :: 3' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.57 kcal/mole Base Pairs 2	·
5 TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : ::: 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -1.47 kcal/mole Base Pairs 2	
5 ' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG 3 ' GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
Delta G -0.96 kcal/mole Base Pairs 2	•
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : 3 GAGGACCGAAGTTTCGGGTTGCTGATCGATAGGCT	
For questions regarding the Dimer Analysis contact our Technical Support Group	

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والمراوية والمرا	प्रपत्नम् प्रकारम् इत्र प्राप्त प्रमुक्तानः स्थाप्तान्त्रपुर्वभूष्याः प्रमुक्तिन्त्रम् स्थित्वक्षाम् कृतिस्थान स्थापन	
Instructions Definitions Feedback		
IDT Y SciTools	•	
OligoAnalyzer 3.0		
# Bases		ANALYZE
5'-TCG GAT AGC TAG TCG TTG GGC TTT GAA GCC AGG AG	Target Type DNA ▼	HAIRPIN
	Oligo Cons	SELF-DIMER
	Total Pin	HETERO-DIMER
c-i	Na ⁺ Conc 50 mM	NCBI BLAST
	3'	TM MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	
,		
Primary Sequence 5'- TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG -3'		
Secondary Sequence		
5'- TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA -3'		
Maximum Delta G -70.77 kcal/mole		
Delta G -8.26 kcal/mole		
Base Pairs 6		
	·	
5' TCGGATAGCTAGTCGTTGGGCTT	TGAAGCCAGGAG	
:: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		•
•		
, Delta G -6.9 kcal/mole		
Base Pairs 4		
F.L. magazimi gamzamagamagagamagazi 2002.202.202.20		
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : :		•
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAG	GCT	•

Delta G -5.7 kcal/mole

•	: : ::: TCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G Base Pairs	-5.02 kcal/mole 3	
5' TCGGAT	PAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : :: :: ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G Base Pairs	-4.74 kcal/mole 3	
5' 3' ATCGCA	TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : :: : AGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G Base Pairs	-4.74 kcal/mole 3	
::	SATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG :: : : AGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G Base Pairs	-4.74 kcal/mole 3	
5' TCGGAT	PAGCTAGTCGTTGGGCTTTGAAGCCAGGAG ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G Base Pairs	-4.16 kcal/mole	
5' 3' ATCGCA	TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : : AAGGATATTTTGGTAAGTGCTGATCGATAGGCT	

Delta G -3.61 kcal/mole

5'	TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
	il en
אייטריים א	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
3 AICGCA	AGGATATTTTGGTAAGTGCTGATTCGATTAGCT
	-3.14 kcal/mole
Base Pairs	2
F	AGCTAGTCGTTGGGCTTTGAAGCCAGGAG
5 TCGGA1	·
_	
3 '	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-3.07 kcal/mole
Base Pairs	2
. .	TO COLUMN COMPA OTTO COMPANIO A A COLUMN COL
5'	TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
3' ATCGCA	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-3.07 kcal/mole
Base Pairs	2
5' TCGGAT	AGCTAGTCGTTGGGCTTTGAAGCCAGGAG
	: :
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-2.56 kcal/mole
Base Pairs	3
_	
	AGCTAGTCGTTGGGCTTTGAAGCCAGGAG
: : :	\cdot
3' ATCGCA	AGGATATTTTGGTAAGTGCTGATCGATAGGCT
······	
Delta G	-2.56 kcal/mole
Base Pairs	3
5' TCGGAT	AGCTAGTCGTTGGGCTTTGAAGCCAGGAG
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -1.95 kcal/mole Base Pairs 2

5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG				
: ::				
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT				
Delta G -1.94 kcal/mole	•			
Base Pairs 2				
			•	
5 · TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG			•	
•				
:: :: : ::				
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT				
			•	
- 1 4.04 Lockback				
Delta G -1.94 kcal/mole				
Base Pairs 2				
		•		
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG				
:::				
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT			•	
	•			
	•			
Delta G -1.94 kcal/mole				
Base Pairs 2				
5				
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG				
: : : : : : : : : : : : : : : : : : : :				
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT				
•				
- 10				
Delta G -1.94 kcal/mole Base Pairs 2				
dase rails 2				
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG				
: : : :				
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		•		
•				
•				
Delta G -1.94 kcal/mole				
Base Pairs 2				
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG				
: : : :				
: : : : 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGG	ርጥ			
, ATCOCHAGOMINITITIGGIANG GCTGATCGATAGG	~ -			

5 TCGGATAGCTAGTCGTTGGGCCTTTGAAGCCAGGAG
: :
ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
The Control of Charles
Delta G -1.6 kcal/mole Base Pairs 2
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.6 kcal/mole Base Pairs 2
Dase Falls 2
5' TCGGATAGCTAGTCGTTGGAGCCAGGAG
3' ATCGCAAGGATATTTTGGTAAGTGCTGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG : : : :
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
5 · TCGGATAGCTAGTCGTTGGAGCCAGGAG
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
5 TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG

```
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
           TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
             :::::||
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.57 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
       ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
                               TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
5 '
                                    11
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.47 kcal/mole
Base Pairs 2
۱ 5
                 {\tt TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG}
                     3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -1.34 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG
                            : : :
          ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
```

Delta G

Base Pairs 2

-1.57 kcal/mole

Delta G -0.96 kcal/mole Base Pairs 2

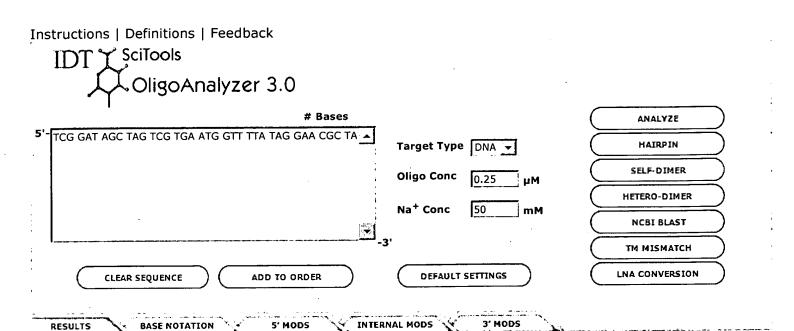
TCGGATAGCTAGTCGTTGGGCTTTGAAGCCAGGAG

: || :

3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

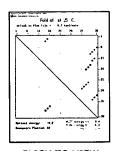
For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com

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mFold Input

General Information



Sequence Name: 38 Base Oligo

Batch Date: 11/8/2006

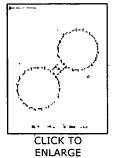
Sequence:

TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA

ADD TO ORDER

CLICK TO VIEW DOT PLOT

Structure 1



ΔG -0.2 kcal.mole⁻¹

T_M 27.4 ℃

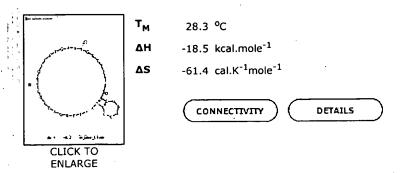
ΔH -25.1 kcal.mole⁻¹

ΔS -83.5 cal.K⁻¹mole⁻¹

CONNECTIVITY

DETAILS

Structure 2



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۱ 3

Instructions Definitions Feedback		
IDT X SciTools	•	
OligoAnalyzer 3.0		
# Bases		ANALYZE
5'-TCG GAT AGC TAG TCG TGA ATG GTT TTA TAG GAA CGC TA	Target Type DNA	HAIRPIN
	Oligo Conc 0.25 µM	SELF-DIMER
		HETERO-DIMER
	Na ⁺ Conc 50 mM	NCBI BLAST
)'	TN MISMATCH
CLEAR SEQUENCE ADD TO ORDER	DEFAULT SETTINGS	LNA CONVERSION
	وبعقي حرم ومعجم أنما مادام	
RESULTS BASE NOTATION 5' MODS INTER	NAL MODS 3' MODS	
	•	
HOMO-DIMER ANALYSIS		
Dimer Sequence		
5'- TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA -3'		
Maximum Delta G -70.41 kcal/mole		
	·	
Delta G -8.26 kcal/mole Base Pairs 6		
•		
5 ' TCGGATAGCTAGTCGTGAATGGTT	TTTATAGGAACGCTA	
:: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
Delta G -5.7 kcal/mole Base Pairs 4	•	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
: :: :: ::::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
Delta G -4.95 kcal/mole Base Pairs 3		
Buse runs 5	,	
5 · TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		

ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Base Pairs 4
TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
: : 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -3.61 kcal/mole
Base Pairs 2
TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -3.61 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
: : : :
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -3.61 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
:: :: :: :: :: :: :: :: :: :: :: :: :
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -3.61 kcal/mole Base Pairs 2
base rails 2
5 TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
: : ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
A CGCAAGGATATTTGGTAAGTGCTGATAGGCT
Delta G -3.4 kcal/mole
Base Pairs 4
5 ' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G

-4.16 kcal/mole

Delta G -3.29 kcal/mole Base Pairs 3	
5 TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA : ::: : 3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -3.14 kcal/mole Base Pairs 2	·
5 · TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA 3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT .	
Delta G -2.56 kcal/mole Base Pairs 3	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA ::: :: ::: : 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -2.56 kcal/mole Base Pairs 3	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA : : ::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	
Delta G -2.56 kcal/mole Base Pairs 3	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA ::: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	·
Delta G -2.44 kcal/mole Base Pairs 3	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA :: :: :: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT	

5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
: : : :: : : : : : : : : : : : : :		
ATCCCAGGATATTTGGTAMGTGCTGATTGGCT		
Delta G -1.94 kcal/mole		
Base Pairs 2		
5 TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		•
: : :: : : : : : : : : : : : : : :		
Delta G -1.94 kcal/mole		
Base Pairs 2	•	
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
: :: :: :		
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATAGGCT		
Delta G -1.94 kcal/mole Base Pairs 2		
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
:: :: ::		
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
		· · · · · · · · · · · · · · · · · · ·
Delta G -1.57 kcal/mole		
Base Pairs 2		
5 ' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
:: 3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		
Delta G -1.57 kcal/mole		
Base Pairs 2		
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA		
::		
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT		•

-1.94 kcal/mole

-1.57 kcal/mole

Delta G -1 Base Pairs 2

Delta G -1 Base Pairs 2

5'	TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3' ATCGC	AAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-1.57 kcal/mole
Base Pairs	2
5 '	TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
J	: : : : : : : :
3' ATTCCC	AAGGATATTTTGGTAAGTGCTGATCGATAGGCT
J ATCCC	
Delta G	-1.57 kcal/mole
Base Pairs	
	•
5' TCGGA	PAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
	-1.47 kcal/mole
Base Pairs	
5'	TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3 ' ATCGC	AAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G	-1.47 kcal/mole
Base Pairs	2
5 '	TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3	
3 י אידרכיר	AAGGATATTTTGGTAAGTGCTGATCGATAGGCT
5 211000	
Delta G	-1.47 kcal/mole
Base Pairs	·
5' TCGGA	TAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
_	::
3'	ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT

Delta G -1.34 kcal/mole Base Pairs 2

5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -0.96 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
: :
3' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT .
Delta G -0.96 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
; ; ; ; ; ;
3 ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -0.96 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
: :: :: : ::
3 ' ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
Delta G -0.96 kcal/mole
Base Pairs 2
5 TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
·
Delta G -0.96 kcal/mole
Base Pairs 2
5' TCGGATAGCTAGTCGTGAATGGTTTTATAGGAACGCTA
3 · ATCGCAAGGATATTTTGGTAAGTGCTGATCGATAGGCT
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For questions regarding the Dimer Analysis contact our Technical Support Group 1-800-328-2661 or e-mail TechSupport@idtdna.com